

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number:113138

TO: Rita Mitra

Location:

Art Unit: 1653

Friday, January 30, 2004

Case Serial Number: (10/032950)

From: Toby Port

Location: Biotech-Chem Library

CM1-6A04

Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Mitra,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port





STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor Remsen Bldg. 01 D86 571-272-2507

Voluntary Results Feedback Form

~	I am an examiner in Workgroup: Example: 1610
>.	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	 Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Со	mments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



=> file caplus; d que 113; d que 116; d que 118; d que 121; d que 124; d que 125; d que 126
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FILE COVERS 1907 - 30 Jan 2004 VOL 140 ISS 6 FILE LAST UPDATED: 29 Jan 2004 (20040129/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

L3 L4			FILE=CAPLUS FILE=CAPLUS		PLU=ON PLU=ON	STAPHYLOCOCCUS AUREUS/CT PROTEINS/CT
L5			FILE=CAPLUS		PLU=ON	PEPTIDES/CW
L6			FILE=CAPLUS		PLU=ON	ANTIBACTERIAL AGENTS+OLD/CT
L7			FILE=CAPLUS		PLU=ON	(L4 OR L5) (L) (PREP OR SPN OR
ш,	002)/RL	ADD-ON	FLU-ON	(L4 OK L3) (L) (FREP OR SPN OR
L12	155		FILE=CAPLUS	7 DD-ON	DI II—ON	/IA OD IEV /IV CVCIO
L13			FILE=CAPLUS		PLU=ON	(L4 OR L5) (L) CYCL? L3 AND L7 AND L12 AND L6
כדנו		TO SEA	LILE-CAPLOS	ABB=ON	PLU=ON	TO AND TI AND TIS AND TO
L3	215	84 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	STAPHYLOCOCCUS AUREUS/CT
L4	7005	10 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	PROTEINS/CT
L5	1176	19 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	PEPTIDES/CW
L6	724	87 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	ANTIBACTERIAL AGENTS+OLD/CT
L7	803	87 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	(L4 OR L5) (L) (PREP OR SPN OR
		THU)/RL			
L10	940	92 SEA	FILE=CAPLUS	ABB=ON	PLU≔ON	LACTAM OR LACTONE
L12	155	22 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	(L4 OR L5) (L) CYCL?
L13		13 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	L3 AND L7 AND L12 AND L6
L14		14 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	L3 AND (L7 OR L12) AND L10
L15		13 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	L14 NOT L13
L16		1 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	L15 AND DIRECTED/TI
L3	215	84 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	STAPHYLOCOCCUS AUREUS/CT
L4	7005	10 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	PROTEINS/CT
L5	1176	19 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	PEPTIDES/CW
L11			FILE=CAPLUS		PLU=ON	AGR
L12	155	22 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	(L4 OR L5) (L) CYCL?
L18	,	3 SEA	FILE=CAPLUS	ABB=ON	PLU=ON	L3 AND L11 AND L12

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L3
          21584 SEA FILE=CAPLUS ABB=ON
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         700510 SEA FILE=CAPLUS ABB=ON
L4
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                                                PROTEINS/CT
L_5
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                                                PEPTIDES/CW
L10
          94092 SEA FILE=CAPLUS ABB=ON
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                                                LACTAM OR LACTONE
L11
           2682 SEA FILE=CAPLUS ABB=ON
                                        PLU=ON
                                                AGR
L12
          15522 SEA FILE=CAPLUS ABB=ON
                                        PLU=ON
                                                (L4 OR L5) (L) CYCL?
              3 SEA FILE=CAPLUS ABB=ON
L18
                                        PLU=ON L3 AND L11 AND L12
L20
              2 SEA FILE=CAPLUS ABB=ON
                                        PLU=ON L3 AND L11 AND ((L4 OR L5) OR
                CYCL?) AND L10
              2 SEA FILE=CAPLUS ABB=ON
L21
                                        PLU=ON L20 NOT L18
L3
          21584 SEA FILE=CAPLUS ABB=ON
                                        PLU=ON
                                                STAPHYLOCOCCUS AUREUS/CT
L4
         700510 SEA FILE=CAPLUS ABB=ON
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                                                PROTEINS/CT
L5
         117619 SEA FILE=CAPLUS ABB=ON
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                                                PEPTIDES/CW
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L12
                                        PLU=ON
                                                (L4 OR L5) (L) CYCL?
L22
             69 SEA FILE=CAPLUS ABB=ON
                                        PLU=ON
                                                ACCESSORY GENE REGULAT?
L24
             0 SEA FILE=CAPLUS ABB=ON
                                        PLU=ON
                                                L3 AND L22 AND L12
                                        PLU=ON
                                                STAPHYLOCOCCUS AUREUS/CT
T.3
          21584 SEA FILE=CAPLUS ABB=ON
          72487 SEA FILE=CAPLUS ABB=ON
                                        PLU=ON ANTIBACTERIAL AGENTS+OLD/CT
L6
L22
             69 SEA FILE=CAPLUS ABB=ON
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L25
              O SEA FILE=CAPLUS ABB=ON
                                        PLU=ON L3 AND L22 AND L6
        21584 SEA FILE=CAPLUS ABB=ON
L3
                                        PLU=ON STAPHYLOCOCCUS AUREUS/CT
L10
          94092 SEA FILE=CAPLUS ABB=ON
                                        PLU=ON
                                               LACTAM OR LACTONE
             69 SEA FILE=CAPLUS ABB=ON
L22
                                        PLU=ON ACCESSORY GENE REGULAT?
L26
             O SEA FILE=CAPLUS ABB=ON
                                        PLU=ON L3 AND L22 AND L10
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=> file medline; d que 135; d que 137; d que 138 FILE 'MEDLINE' ENTERED AT 17:34:18 ON 30 JAN 2004

FILE LAST UPDATED: 29 JAN 2004 (20040129/UP). FILE COVERS 1958 TO DATE.

On December 14, 2003, the 2004 MeSH terms were loaded. See HELP RLOAD for details.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2004 vocabulary. See http://www.nlm.nih.gov/mesh/ and http:\\www.nih.gov/pubs/yechbull/nd03/nd03_mesh.html for a description on changes.

This file contains CAS Registry Numbers for easy and accurate substance identification.

L28	24379	SEA FILE=MEDLINE ABB=ON PLU=ON STAPHYLOCOCCUS AUREUS/CT	
L29	497	SEA FILE=MEDLINE ABB=ON PLU=ON AGR OR ACCESSORY GENE	
		REGULAT?	
L30	107060	SEA FILE=MEDLINE ABB=ON PLU=ON ANTI-BACTERIAL AGENTS/CT OF	3
		ANTI-INFECTIVE AGENTS/CT	
L35	5	SEA FILE=MEDLINE ABB=ON PLU=ON L28 AND L29 AND L30	

L28	24379	SEA FILE=MEDLINE	ABB=ON PLU=ON	STAPHYLOCOCCUS AUREUS/CT
L29	497	SEA FILE=MEDLINE	ABB=ON PLU=ON	AGR OR ACCESSORY GENE
•		REGULAT?		
L31	354100	SEA FILE=MEDLINE	ABB=ON PLU=ON	CYCLIC (3A) PROTEIN OR
		PEPTIDE		
L33	56475	SEA FILE=MEDLINE	ABB=ON PLU=ON	LACTONES+NT/CT
L37	2	SEA FILE=MEDLINE	ABB=ON PLU=ON	L28 AND L29 AND L31 AND L33
				·
L28	24379	SEA FILE=MEDLINE	ABB=ON PLU=ON	STAPHYLOCOCCUS AUREUS/CT
L29	497	SEA FILE=MEDLINE	ABB=ON PLU=ON	AGR OR ACCESSORY GENE
		REGULAT?		
L31	354100	SEA FILE=MEDLINE	ABB=ON PLU=ON	CYCLIC (3A) PROTEIN OR
		PEPTIDE		
L34	72703	SEA FILE=MEDLINE	ABB=ON PLU=ON	LACTAMS+NT/CT
L38	3	SEA FILE=MEDLINE	ABB=ON PLU=ON	L28 AND L29 AND L31 AND L34

=> 's 135 or 137 or 138 L73 9 L35 OR L37 OR L38

=> file embase; d que 148; d que 149; d que 150 FILE 'EMBASE' ENTERED AT 17:34:59 ON 30 JAN 2004 COPYRIGHT (C) 2004 Elsevier Inc. All rights reserved.

FILE COVERS 1974 TO 29 Jan 2004 (20040129/ED)

EMBASE has been reloaded. Enter HELP RLOAD for details.

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L39	35935	SEA FILE=EMBASE	ABB=ON	PLU=ON	"STAPHYLOCOCCUS AUREUS"+ALL/CT
L40 L41	838278 363	SEA FILE=EMBASE SEA FILE=EMBASE		PLU=ON PLU=ON	ANTIINFECTIVE AGENT+NT/CT AGR OR ACCESSORY GENE REGULAT?
L42	30871	SEA FILE=EMBASE CYCL?	ABB=ON	PLU=ON	(PROTEIN OR PEPTIDE) (3A)
L48	0	SEA FILE=EMBASE	ABB=ON	PLU=ON	L39 AND L41 AND L40 AND L42
L39	35935	SEA FILE=EMBASE	ABB=ON	PLU=ON	"STAPHYLOCOCCUS AUREUS"+ALL/CT
L40 L41	838278 363			PLU=ON PLU=ON	ANTIINFECTIVE AGENT+NT/CT AGR OR ACCESSORY GENE REGULAT?
L44 L45 L49	4193 7912 0	SEA FILE=EMBASE SEA FILE=EMBASE SEA FILE=EMBASE OR L45)	ABB=ON	PLU=ON PLU=ON PLU=ON	LACTAM+NT/CT LACTONE+NT/CT L39 AND L41 AND L40 AND (L44
L39	35935	SEA FILE=EMBASE	ABB=ON	PLU=ON	"STAPHYLOCOCCUS AUREUS"+ALL/CT

L40	838278 SE	EA FILE=EMBASE ABB=ON	PLU=ON	ANTIINFECTIVE AGENT+NT/CT
L41	363 SE	EA FILE=EMBASE ABB=ON	PLU=ON	AGR OR ACCESSORY GENE REGULAT?
L50	0 SE	EA FILE=EMBASE ABB=ON	PLU=ON	L39 AND L41 AND L40 AND CYCL?

=> file wpid; d que 157; d que 158; d que 160 FILE 'WPIDS' ENTERED AT 17:35:16 ON 30 JAN 2004 COPYRIGHT (C) 2004 THOMSON DERWENT

28 JAN 2004 <20040128/UP> FILE LAST UPDATED: MOST RECENT DERWENT UPDATE: 200407 <200407/DW> DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

- >>> NEW WEEKLY SDI FREQUENCY AVAILABLE --> see NEWS <><
- >>> PATENT IMAGES AVAILABLE FOR PRINT AND DISPLAY <<<

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- >>> FOR DETAILS OF THE PATENTS COVERED IN CURRENT UPDATES, SEE http://thomsonderwent.com/coverage/latestupdates/ <<<
- >>> FOR INFORMATION ON ALL DERWENT WORLD PATENTS INDEX USER GUIDES, PLEASE VISIT: http://thomsonderwent.com/support/userguides/ <<<
- >>> ADDITIONAL POLYMER INDEXING CODES WILL BE IMPLEMENTED FROM DERWENT UPDATE 200403. THE TIME RANGE CODE WILL ALSO CHANGE FROM 018 TO 2004. SDIS USING THE TIME RANGE CODE WILL NEED TO BE UPDATED. FOR FURTHER DETAILS: http://thomsonderwent.com/chem/polymers/ <<<

L51 L52 L53 L54	3758 1246 92 48087	SEA SEA SEA	FILE=WPIDS FILE=WPIDS FILE=WPIDS FILE=WPIDS PERICID? OR	ABB=ON ABB=ON ABB=ON	PLU=ON PLU=ON PLU=ON PLU=ON PLU=ON	STAPHYLOCOCCUS AUREUS S AUREUS AGR OR ACCESSORY GENE REGULAT? ANTIBACTER? OR ANTIINFECT? OR R? OR INFECT?)
L57	7		FILE=WPIDS		PLU=ON	(L51 OR L52) AND L53 AND L54
L51	3758	SEA	FILE=WPIDS	ABB=ON	PLU=ON	STAPHYLOCOCCUS AUREUS
L52	1246	SEA	FILE=WPIDS	ABB=ON	PLU=ON	S AUREUS
L53	92	SEA	FILE=WPIDS	ABB=ON	PLU=ON	AGR OR ACCESSORY GENE REGULAT?
L55	19291	SEA	FILE=WPIDS	ABB=ON	PLU=ON	LACTAM OR LACTONE
L58	2	SEA	FILE=WPIDS	ABB=ON	PLU=ON	(L51 OR L52) AND L53 AND L55
L51	3758	SEA	FILE=WPIDS	ABB=ON	PLU=ON	STAPHYLOCOCCUS AUREUS
L52	1246	SEA	FILE=WPIDS		PLU=ON	S AUREUS
L53	92	SEA	11111	ABB=ON	PLU=ON	AGR OR ACCESSORY GENE REGULAT?
L56	2040	SEA	FILE=WPIDS	ABB=ON	PLU=ON	(PEPTIDE OR PROTEIN) (3A) CYCL?

L60 4 SEA FILE=WPIDS ABB=ON PLU=ON (L51 OR L52) AND L53 AND L56

=> s 157 or 158 or 160 L74 7 L57 OR L58 OR L60

=> file biosis; d que 168; d que 171 FILE 'BIOSIS' ENTERED AT 17:35:48 ON 30 JAN 2004 COPYRIGHT (C) 2004 BIOLOGICAL ABSTRACTS INC.(R)

FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 28 January 2004 (20040128/ED)

FILE RELOADED: 19 October 2003.

L62 60064 SEA FILE=BIOSIS ABB=ON PLU=ON (STA	APHYLOCOCCUS OR STAPH OR S)
	OR ACCESSORY GENE REGULAT?
L64 204285 SEA FILE=BIOSIS ABB=ON PLU=ON ANTI ANTI (W) (BACTER? OR INFECT?) OR BAC	BACTER? OR ANTIINFECT? OR CTERICID?
L67 26 SEA FILE=BIOSIS ABB=ON PLU=ON L62	AND L63 AND L64
L68 1 SEA FILE=BIOSIS ABB=ON PLU=ON L67	AND ENGINEERED/TI
L62 60064 SEA FILE=BIOSIS ABB=ON PLU=ON (STA	APHYLOCOCCUS OR STAPH OR S)
L63 604 SEA FILE=BIOSIS ABB=ON PLU=ON AGR	OR ACCESSORY GENE REGULAT?
L66 29093 SEA FILE=BIOSIS ABB=ON PLU=ON LACT	TONE OR LACTAM
	AND L63 AND L66
D/O . O OD: 1220 000000	AND EVOLUTION/TI

=> dup rem 173 172 175 174 FILE 'MEDLINE' ENTERED AT 17:36:22 ON 30 JAN 2004

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PROCESSING COMPLETED FOR L73
PROCESSING COMPLETED FOR L72
PROCESSING COMPLETED FOR L75
PROCESSING COMPLETED FOR L74
L76
34 DUP REM L73 L72 L75 L74 (3 DUPLICATES REMOVED)
ANSWERS '1-9' FROM FILE MEDLINE

ANSWERS '10-27' FROM FILE CAPLUS ANSWER '28' FROM FILE BIOSIS ANSWERS '29-34' FROM FILE WPIDS

=> d ibib ab 176 1-34

L76 ANSWER 1 OF 34 MEDLINE on STN DUPLICATE 2

ACCESSION NUMBER:

2001444137 MEDLINE

DOCUMENT NUMBER:

PubMed ID: 11489134 21382775

TITLE:

Structure, activity and evolution of the group I thiolactone peptide quorum-sensing system of

Staphylococcus aureus.

AUTHOR:

MDowell P; Affas Z; Reynolds C; Holden M T; Wood S J; Saint S; Cockayne A; Hill P J; Dodd C E; Bycroft B W; Chan W C;

Williams P

CORPORATE SOURCE:

Institute of Infections and Immunity, School of Pharmaceutical Sciences, and School of BioSciences, University of Nottingham, Nottingham NG7 2RD, UK. MOLECULAR MICROBIOLOGY, (2001 Jul) 41 (2) 503-12. Journal code: 8712028. ISSN: 0950-382X.

SOURCE:

PUB. COUNTRY:

England: United Kingdom

DOCUMENT TYPE:

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

FILE SEGMENT:

English Priority Journals

OTHER SOURCE:

GENBANK-AF001782; GENBANK-AF001783

ENTRY MONTH:

200204

ENTRY DATE:

Entered STN: 20010813

Last Updated on STN: 20020412

Entered Medline: 20020411

AΒ In Staphylococcus aureus, the agr locus is responsible for controlling virulence gene expression via quorum sensing. As the blockade of quorum sensing offers a novel strategy for attenuating infection, we sought to gain novel insights into the structure, activity and turnover of the secreted staphylococcal autoinducing peptide (AIP) signal molecules. A series of analogues (including the L-alanine and D-amino acid scanned peptides) was synthesized to determine the functionally critical residues within the S. aureus group I AIP. As a consequence, we established that (i) the group I AIP is inactivated in culture supernatants by the formation of the corresponding methionyl sulphoxide; and (ii) the group I AIP lactam analogue retains the capacity to activate agr, suggesting that covalent modification of the AgrC receptor is not a necessary prerequisite for agr activation. Although each of the D-amino acid scanned AIP analogues retained activity, replacement of the endocyclic amino acid residue (aspartate) located C-terminally to the central cysteine with alanine converted the group I AIP from an activator to a potent inhibitor. The screening of clinical S. aureus isolates for novel AIP groups revealed a variant that differed from the group I AIP by a single amino acid residue (aspartate to tyrosine) in the same position defined as critical by alanine scanning. Although this AIP inhibits group I S. aureus strains, the producer strains possess a functional agr locus dependent on the endogenous peptide and, as such, constitute a fourth S. aureus AIP pheromone group (group IV). The addition of exogenous synthetic AIPs to S. aureus inhibited the production of toxic shock syndrome toxin (TSST-1) and enterotoxin C3, confirming the potential of quorum-sensing blockade as a therapeutic strategy.

L76 ANSWER 2 OF 34

MEDLINE on STN

DUPLICATE 3

ACCESSION NUMBER:

1999145530 MEDLINE

DOCUMENT NUMBER:

99145530 PubMed ID: 9990004

TITLE:

Structure-activity analysis of synthetic autoinducing

thiolactone peptides from Staphylococcus aureus

responsible for virulence.

AUTHOR: Mayville P; Ji G; Beavis R; Yang H; Goger M; Novick R P;

Muir T W

CORPORATE SOURCE: Laboratory of Synthetic Protein Chemistry, The Rockefeller

University, 1230 York Avenue, New York, NY 10021, USA.

CONTRACT NUMBER: A142783 (NIAID)

AI30138-09 (NIGMS)

GM55843-01

PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE SOURCE:

UNITED STATES OF AMERICA, (1999 Feb 16) 96 (4) 1218-23.

Journal code: 7505876. ISSN: 0027-8424.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199903

ENTRY DATE: Entered STN: 19990402

> Last Updated on STN: 19990402 Entered Medline: 19990325

The synthesis of virulence factors and other extracellular proteins AB responsible for pathogenicity in Staphylococcus aureus is under the control of the agr locus. A secreted agr-encoded peptide, AgrD, processed from the AgrD gene product, is known to be an effector of self-strain activation and cross-strain inhibition of the agr response. Biochemical analysis of AgrD peptides isolated from culture supernatants has suggested that they contain an unusual thiol ester-linked cyclic structure. In the present work, chemical synthesis is used to confirm that the mature AgrD peptides contain a thiolactone structure and that this feature is absolutely necessary for full biological activity. The AgrD synthetic thiolactone peptides exhibited biological activity in vivo in a mouse protection test. Structure-activity studies have allowed key aspects of the peptide structure involved in the differential activation and inhibition functions to be identified. Accordingly, we propose a model for activation and inhibition of the agr

L76 ANSWER 3 OF 34 MEDLINE on STN ACCESSION NUMBER: 2003145749 MEDLINE

DOCUMENT NUMBER: 22546994 PubMed ID: 12660939

TITLE: Staphylococcus aureus accessory gene regulator (agr) group II: is there a

acylation of the agr transmembrane receptor, AgrC.

relationship to the development of intermediate-level

glycopeptide resistance?.

AUTHOR: Sakoulas George; Eliopoulos George M; Moellering Robert C

response in which the former, but not the latter, involves specific

Jr; Novick Richard P; Venkataraman Lata; Wennersten Christine; DeGirolami Paola C; Schwaber Mitchell J; Gold

Howard S

CORPORATE SOURCE: Department of Medicine, Division of Laboratory and

> Transfusion Medicine and Harvard Medical School, Boston, Massachussetts, USA.. gsakoulas@crystalrunhealthcare.com

SOURCE: JOURNAL OF INFECTIOUS DISEASES, (2003 Mar 15) 187 (6)

929-38.

Journal code: 0413675. ISSN: 0022-1899.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

DOCUMENT TYPE: LANGUAGE:

English

FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals

ENTRY MONTH: 200304 ENTRY DATE:

Entered STN: 20030331

Last Updated on STN: 20030426 Entered Medline: 20030425

AB We previously determined that all 6 Staphylococcus aureus strains with confirmed intermediate-level resistance to glycopeptides (glycopeptide intermediate S. aureus [GISA]) from the United States that we tested belonged to accessory gene regulator (
agr) group II. In the present study, we found that 56% of surveyed bloodstream methicillin-resistant S. aureus isolates (n = 148) at

our hospital were $\operatorname{\mathbf{agr}}$ group II, whereas only 24% of methicillin-susceptible S. aureus isolates (n = 33) were $\operatorname{\mathbf{agr}}$ group II (P = .001). Population analysis of genetically engineered $\operatorname{\mathbf{agr}}$ -null and parent wild-type strains of groups I, II, and IV

revealed that, when agr function is lost, the agr group II knockout S. aureus was most likely to develop glycopeptide

heteroresistance after growth in 1 microg/mL but not 16 microg/mL vancomycin. This strain was unique in showing decreased autolysis after growth in these conditions. This study suggests that some S. aureus strains have an intrinsic survival advantage under a glycopeptide selective pressure, which is possibly related to reduced autolysis after exposure to subinhibitory concentrations of glycopeptide.

L76 ANSWER 4 OF 34 MEDLINE on STN ACCESSION NUMBER: 2003333177 MEDLINE DOCUMENT NUMBER: PubMed ID: 12865410

TITLE:

Salicylic acid attenuates virulence in endovascular infections by targeting global regulatory pathways in

Staphylococcus aureus.

COMMENT:

Comment in: J Clin Invest. 2003 Jul;112(2):149-51. PubMed

ID: 12865403

AUTHOR:

Kupferwasser Leon Iri; Yeaman Michael R; Nast Cynthia C; Kupferwasser Deborah; Xiong Yan-Qiong; Palma Marco; Cheung

Ambrose L; Bayer Arnold S

CORPORATE SOURCE:

Division of Infectious Disease, Harbor-UCLA (University of

California-Los Angeles), Torrance, California, USA.

CONTRACT NUMBER:

A: AI-37142 (NIAID)

AI-39001 (NIAID) AI-39108 (NIAID)

SOURCE:

Journal of clinical investigation, (2003 Jul) 112 (2)

222-33.

Journal code: 7802877. ISSN: 0021-9738.

PUB. COUNTRY:

United States

DOCUMENT TYPE:

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Abridged Index Medicus Journals; Priority Journals

ENTRY MONTH:

200308

ENTRY DATE:

Entered STN: 20030717

Last Updated on STN: 20030807 Entered Medline: 20030806

Aspirin has been previously shown to reduce the in vivo virulence of Staphylococcus aureus in experimental endocarditis, through antiplatelet and antimicrobial mechanisms. In the present study, salicylic acid, the major in vivo metabolite of aspirin, mitigated two important virulence phenotypes in both clinical and laboratory S. aureus strains: alpha-hemolysin secretion and fibronectin binding in vitro. In addition, salicylic acid reduced the expression of the alpha-hemolysin gene promoter, hla, and the fibronectin gene promoter, fnbA. Transcriptional analysis, fluorometry, and flow cytometry revealed evidence of salicylic acid-mediated activation of the stress-response gene sigB. Expression of the sigB-repressible global regulon sarA and the global regulon agr were also mitigated by salicylic acid, corresponding to the

reduced expression of the hla and fnbA genes in vitro. Studies in experimental endocarditis confirmed the key roles of both sarA and sigB in mediating the antistaphylococcal effects of salicylic acid in vivo. Therefore, aspirin has the potential to be an adjuvant therapeutic agent against endovascular infections that result from S. aureus, by downmodulating key staphylococcal global regulons and structural genes in vivo, thus abrogating relevant virulence phenotypes.

MEDLINE on STN L76 ANSWER 5 OF 34

ACCESSION NUMBER: 2001248100 MEDLINE

DOCUMENT NUMBER: 21189213 PubMed ID: 11292717

TITLE: Subinhibitory clindamycin differentially inhibits

transcription of exoprotein genes in Staphylococcus aureus.

AUTHOR: Herbert S; Barry P; Novick R P

Program in Molecular Pathogenesis, Skirball Institute, New CORPORATE SOURCE:

York University School of Medicine, New York, New York

10016, USA.

CONTRACT NUMBER: RO1-AI30138 (NIAID)

INFECTION AND IMMUNITY, (2001 May) 69 (5) 2996-3003. SOURCE:

Journal code: 0246127. ISSN: 0019-9567.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

English LANGUAGE:

Priority Journals FILE SEGMENT:

ENTRY MONTH: 200105

ENTRY DATE: Entered STN: 20010517

> Last Updated on STN: 20010517 Entered Medline: 20010510

AB It has long been known that certain antibiotics, at subinhibitory concentrations, differentially inhibit the synthesis of alpha-hemolysin and other staphylococcal virulence factors. In this report, we show that subinhibitory clindamycin (SBCL) eliminates production of nearly all exoproteins by Staphylococcus aureus but has virtually no effect on cytoplasmic proteins. The effect was abolished by a gene conferring resistance to macrolides-lincosamides-streptogramin B, showing that differential inhibition of protein synthesis is responsible; remarkably, however, subinhibitory clindamycin blocked production of several of the individual exoprotein genes, including spa (encoding protein A), hla (encoding alpha-hemolysin), and spr (encoding serine protease), at the level of transcription, suggesting that the primary effect must be differential inhibition of the synthesis of one or more regulatory proteins. In contrast to earlier reports, however, we found that subinhibitory clindamycin stimulates synthesis of coagulase and fibronectin binding protein B, also at the level of transcription. agr and sar expression was minimally affected by subinhibitory clindamycin. These effects varied from strain to strain and do not seem to be responsible for the effects of subinhibitory clindamycin on the overall exoprotein pattern.

MEDLINE on STN L76 ANSWER 6 OF 34 ACCESSION NUMBER: 2001285436 MEDLINE

PubMed ID: 11179383 DOCUMENT NUMBER: 21117027

Pheromone cross-inhibition between Staphylococcus aureus TITLE:

and Staphylococcus epidermidis.

AUTHOR . Otto M; Echner H; Voelter W; Gotz F

Mikrobielle Genetik, Abteilung fur Physikalische Biochemie, CORPORATE SOURCE:

Universitat Tubingen, Tubingen, Germany...

michael.otto@uni-tuebingen.de

INFECTION AND IMMUNITY, (2001 Mar) 69 (3) 1957-60. Journal code: 0246127. ISSN: 0019-9567. SOURCE:

United States PUB. COUNTRY:

DOCUMENT TYPE:

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

200105

ENTRY DATE:

Entered STN: 20010529

Last Updated on STN: 20010529

Entered Medline: 20010524

AB Cross-inhibition by quorum-sensing pheromones between Staphylococcus aureus and Staphylococcus epidermidis was investigated using all known S. aureus agr pheromone subgroups. All S. aureus subgroups were sensitive towards the S. epidermidis pheromone, with the exception of the recently identified subgroup 4. The subgroup 4 pheromone was also the only S. aureus pheromone able to inhibit the S. epidermidis agr response. The close relation of subgroup 4 to subgroup 1 suggests that subgroup 4 might have evolved from subgroup 1 by mutation under the selective pressure of competition with S. epidermidis. The competition between S. aureus and S. epidermidis by means of quorum-sensing cross talk seems to be generally in favor of S. epidermidis, which might explain the predominance of S. epidermidis on the skin and in infections on indwelling medical devices.

L76 ANSWER 7 OF 34

MEDLINE on STN

ACCESSION NUMBER: DOCUMENT NUMBER:

2001541407 MEDLINE

TITLE:

21472528 PubMed ID: 11587788

Staphylococcus aureus and Staphylococcus epidermidis

peptide pheromones produced by the accessory

gene regulator agr system.

AUTHOR:

Otto M

CORPORATE SOURCE:

Rocky Mountain Laboratory, Laboratory of Human Bacterial Pathogenesis, NIAID, NIH, 903 South 4th Street, Hamilton,

MT 59840, USA.. motto@niaid.nih.gov

SOURCE:

PEPTIDES, (2001 Oct) 22 (10) 1603-8. Ref: 39

Journal code: 8008690. ISSN: 0196-9781.

PUB. COUNTRY:

United States

DOCUMENT TYPE:

Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, TUTORIAL)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

200112

ENTRY DATE:

Entered STN: 20011008

Last Updated on STN: 20020122 Entered Medline: 20011214

AB The accessory gene regulator (agr)

system of staphylococci regulates the expression of virulence factors in response to cell density. The extracellular signaling molecule encoded by this system is a thiolactone-containing pheromone peptide whose primary sequence varies among staphylococcal strains. A post-translational modification of the peptide is believed to be carried out by an enzyme with a novel function, AgrB. Staphylococcal pheromones show cross-inhibiting properties: Pheromones of self and pheromones of non-self induce and suppress the agr response, respectively, and have therefore been proposed as novel anti-staphylococcal drugs. As inhibition of agr leads to diminished expression of toxins, but to increased expression of colonization factors and biofilm formation, their therapeutic potential remains yet to be evaluated in depth.

L76 ANSWER 8 OF 34

MEDLINE on STN

ACCESSION NUMBER:

2001284536 MEDLINE

DOCUMENT NUMBER:

20542125 PubMed ID: 11087872

TITLE:

Rational design of a global inhibitor of the virulence

response in Staphylococcus aureus, based in part on

localization of the site of inhibition to the

receptor-histidine kinase, AgrC.

AUTHOR: Lyon G J; Mayville P; Muir T W; Novick R P

CORPORATE SOURCE: Laboratory of Synthetic Protein Chemistry, The Rockefeller

University, 1230 York Avenue, New York, NY 10021, USA.

CONTRACT NUMBER: AI 42783 (NIAID)

GM07739 (NIGMS)

SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE

UNITED STATES OF AMERICA, (2000 Nov 21) 97 (24) 13330-5.

Journal code: 7505876. ISSN: 0027-8424.

PUB. COUNTRY:

United States

DOCUMENT TYPE:

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

200105

ENTRY DATE:

Entered STN: 20010529

Last Updated on STN: 20010529 Entered Medline: 20010524

AΒ Two-component signaling systems involving receptor-histidine kinases are ubiquitous in bacteria and have been found in yeast and plants. These systems provide the major means by which bacteria communicate with each other and the outside world. Remarkably, very little is known concerning the extracellular ligands that presumably bind to receptor-histidine kinases to initiate signaling. The two-component agr signaling circuit in Staphylococcus aureus is one system where the ligands are known in chemical detail, thus opening the door for detailed structure-activity relationship studies. These ligands are short (8- to 9-aa) peptides containing a thiolactone structure, in which the alpha-carboxyl group of the C-terminal amino acid is linked to the sulfhydryl group of a cysteine, which is always the fifth amino acid from the C terminus of the peptide. One unique aspect of the agr system is that peptides that activate virulence expression in one group of S. aureus strains also inhibit virulence expression in other groups of S. aureus strains. Herein, it is demonstrated by switching the receptor-histidine kinase, AgrC, between strains of different agr specificity types, that intragroup activation and intergroup inhibition are both mediated by the same group-specific receptors. These results have facilitated the development of a global inhibitor of virulence in S. aureus, which consists of a truncated version of one of the naturally occurring thiolactone peptides.

L76 ANSWER 9 OF 34 MEDLINE on STN ACCESSION NUMBER: 2001010995 MEDLINE

DOCUMENT NUMBER:

20461218 PubMed ID: 11004170

TITLE:

Population studies of methicillin-resistant and -sensitive Staphylococcus aureus strains reveal a lack of variability in the agrD gene, encoding a staphylococcal autoinducer

peptide.

AUTHOR:

van Leeuwen W; van Nieuwenhuizen W; Gijzen C; Verbrugh H;

van Belkum A

CORPORATE SOURCE:

Department of Medical Microbiology and Infectious Diseases, Erasmus University Medical Center Rotterdam, Rotterdam, The

Netherlands.. vanleeuwen@bacl.azr.nl

SOURCE:

JOURNAL OF BACTERIOLOGY, (2000 Oct) 182 (20) 5721-9.

Journal code: 2985120R. ISSN: 0021-9193.

PUB. COUNTRY:

United States

DOCUMENT TYPE:

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

200010

ENTRY DATE:

Entered STN: 20010322

Last Updated on STN: 20010322 Entered Medline: 20001026

The virulence of Staphylococcus aureus is controlled by the AΒ

accessory gene regulator (agr)

system, including an extracellular inducer encoded by agrD. Variable agr PCR restriction fragment length polymorphism (RFLP) patterns of unique S. aureus strains (n = 192) were determined for a region comprising agrD and parts of the neighboring agrC and agrB genes. Twelve unique RFLP patterns were identified among S. aureus strains in general; these patterns were further specified by sequencing. All sequences could be catalogued in the three current agr groups. A major proportion of the S. aureus strains belong to agr group 1, whereas only 6% of the methicillin-susceptible S. aureus strains and 5% of the methicillin-resistant S. aureus strains belong to agr groups 2 and 3, respectively. The homology between groups varied from 75 to 80%, and within groups it varied from 96 to 100%. Different levels of sequence variability were observed in the different agr genes. agr-related bacterial interference among colonizing S. aureus strains in the noses of persistent and intermittent human carriers was studied. S. aureus strains belonging to different agr groups were encountered in the same individual. This may suggest that the activity of the agrD gene product does not define colonization dynamics, which is further substantiated by the rarity of agr group 2 and 3 strains.

L76 ANSWER 10 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1

ACCESSION NUMBER:

2002:688473 CAPLUS

DOCUMENT NUMBER:

137:222001

TITLE:

Blocking expression of virulence factors in

Staphylococcus aureus with peptide compositions Novick, Richard P.; Ji, Guangyong; Beavis, Ronald

INVENTOR(S): PATENT ASSIGNEE(S):

SOURCE:

New York University, USA

U.S., 12 pp., Cont.-in-part of U.S. Ser. No. 651,226,

abandoned. CODEN: USXXAM

DOCUMENT TYPE:

LANGUAGE:

Patent

English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

	PATENT NO.	KIND	DATE		APPLICATION NO.	DATE
	US 6447786	В1	20020910		US 1997-861476	19970522
	US 2003078378	A1 -	20030424		US 2002-201444	20020723
PRIO	RITY APPLN. INFO.	:		US	1994-318499 B	2 19941004
				US	1996-651226 В	2 19960522
				US	1997-861476 A	1 19970522

This invention provides peptides which inhibit agr transcription AΒ in S. aureus and thereby block the expression of virulence factors in S. aureus, pharmaceutical compns. comprising these peptides, as well as methods for treating or preventing an infection or disease caused by S. aureus using the peptides of the present invention.

THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS REFERENCE COUNT: 15 RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L76 ANSWER 11 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:

2004:41215 CAPLUS

TITLE: INVENTOR(S): Preparation of nocathiacin O-derivatives Hudyma, Thomas W.; Zheng, Xiaofan; Naidu, B. Narasimhulu; Sorenson, Margaret E.; Regueiro-Ren, Alicia; Connolly, Timothy P.; Matiskella, John D.; Kim, Oak K.; Zhang, Yunhui; Springer, Dane M.; Goodrich, Jason; Ueda, Yasutsugu; Bronson, Joanne J.

Bristol-Myers Squibb Company, USA PATENT ASSIGNEE(S):

PCT Int. Appl., 53 pp. SOURCE:

CODEN: PIXXD2

DOCUMENT TYPE:

LANGUAGE:

Patent English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

	PATENT NO.					ND	DATE		APPLICATION NO. DATE									
	WO	2004	0046	46	A:	2	2004	0115		W	0 20	03-U	S210	12	2003	0702		
		W:	ΑE,	AG,	AL,	ΑM,	ΑT,	ΑU,	AZ,	ΒA,	ΒB,	BG,	BR,	BY,	BZ,	CA,	CH,	CN,
			CO,	CR,	CU,	CZ,	DE,	DK,	DM,	DZ,	EC,	EE,	ES,	FI,	GB,	GD,	GE,	GH,
			GM,	HR,	ΗU,	ID,	IL,	IN,	IS,	JP,	KE,	KG,	ΚP,	KR,	ΚZ,	LC,	LK,	LR,
			LS,	LT,	LU,	LV,	MA,	MD,	MG,	MK,	MN,	MW,	MX,	MΖ,	NΙ,	NO,	NΖ,	OM,
			PG,	PH,	PL,	PΤ,	RO,	RU,	SC,	SD,	SE,	SG,	SK,	SL,	SY,	ТJ,	TM,	TN,
			TR,	TT,	TZ,	UA,	UG,	UZ,	VC,	VN,	YU,	ZA,	ZM,	ZW,	ΑM,	ΑZ,	BY,	KG,
					RU,													
		RW:	GH,	GM,	KE,	LS,	MW,	MΖ,	SD,	SL,	SZ,	TZ,	UG,	ZM,	ZW,	ΑT,	BE,	BG,
							DK,											
			NL,	PT,	RO,	SE,	SI,	SK,	TR,	BF,	ВJ,	CF,	CG,	CI,	CM,	GΑ,	GN,	GQ,
							SN,											
	US	2004	0189	63														
PRIO		APP																
AΒ	The	e inv	enti	on p	rovi	des	comp	ds.	I [Z	= N	H2 o.	r NH	C(:C	H2)C	ONH2	; R1	==	
		nethy																
																		lkenyl,
		cynyl														., Н	,	
		spho																
		H2CH2																
	ant	ibio	tic	acti	vity	, in	clud	ing a	acti	vity	tow	ards	Grai	m-po	s. b	acte.	ria a	and
																		epared by
		nethy																
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	and	d Ent	eroc	occu	s fa	ecal	is,	resp.	•									

L76 ANSWER 12 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:

2003:1007003 CAPLUS

DOCUMENT NUMBER:

INVENTOR(S):

140:59934

TITLE:

Synthesis of cyclic peptide macrolides for use in the

treatment and prevention of bacterial infection Lampe, Thomas; Adelt, Isabelle; Beyer, Dieter; Brunner, Nina; Endermann, Rainer; Ehlert, Kerstin; Kroll, Hein-Peter; Von Nussbaum, Franz; Raddatz,

Siegfried; Rudolph, Joachim; Schiffer, Guido; Schumacher, Andreas; Cancho-Grande, Yolanda; Michels,

Martin; Weigand, Stefan

PATENT ASSIGNEE(S):

Bayer Healthcare A.-G., Germany

SOURCE:

PCT Int. Appl., 190 pp. CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE:

German

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

APPLICATION NO. DATE PATENT NO. KIND DATE

```
WO 2003106480
                                           WO 2003-EP6078
                            20031224
                                                            20030610
                       Α1
         W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM,
             PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT,
             TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ,
             MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
             CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC,
             NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
             GW, ML, MR, NE, SN, TD, TG
                                           DE 2002-10226921 20020617
     DE 10226921
                       Α1
                            20031224
                                        DE 2002-10226921 A 20020617
PRIORITY APPLN. INFO.:
    The invention relates to antibacterial amide macrocycles, e.g. (I), to
    methods for the production thereof, and to the use of the same for producing
    pharmaceuticals for the treatment and/or prophylaxis of illness, especially
    bacterial infections. Title compds. were synthesized beginning with
     salicylaldehyde, which was 5-iodinated, O-protected, reduced to the
    hydroxymethyl, brominated on the CH2 group, and coupled with di-Et
     2-tert-butoxycarbonylaminomalonate, which, after decarboxylation and
    deesterification, gave the (DL)-N-Boc-protected 2'-benzyloxy-5'-iodo-
    phenylalanine (II). II was resolved into its pure D- and L-enantiomers;
     the L-II was protected as the N-Cbz derivative, then esterified with
     2-(trimethylsilyl)ethanol, then reacted with (III) (prepared from II and
     4,4,4',4',5,5,5',5'-octamethyl-2,2'-bi-1,3,2-dioxaborolane) to give
    biphenyl compound (IV). In a sep. reaction, (V) was prepared from the
    corresponding L-ornithine tert-Bu ester, the lactone opened and the alc.
    protected as the tert-butyldimethylsilyl derivative, and reacted with biphenyl
    IV, to give, after deprotection and amide formation, I as the
    dihydrochloride salt. In in vitro tests, using S. aureus, E. faecalis, B.
    catarrhalis, and E. coli strains, I had min. blood concentration effective ranges
    of 0.2-6.25 \mu M.
REFERENCE COUNT:
                               THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS
                               RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
                      CAPLUS COPYRIGHT 2004 ACS on STN
L76 ANSWER 13 OF 34
ACCESSION NUMBER:
                         2003:521316 CAPLUS
                         139:277145
DOCUMENT NUMBER:
                         Side-chain-to-tail thiolactone peptide inhibitors of
TITLE:
                         the staphylococcal quorum-sensing system
                         Scott, R. John; Lian, Lu-Yun; Muharram, S. Hanna;
AUTHOR(S):
                         Cockayne, Alan; Wood, Stewart J.; Bycroft, Barrie W.;
                         Williams, Paul; Chan, Weng C.
                         School of Pharmaceutical Sciences, University of
CORPORATE SOURCE:
                         Nottingham, Nottingham, NG7 2RD, UK
                         Bioorganic & Medicinal Chemistry Letters (2003),
SOURCE:
                         13(15), 2449-2453
CODEN: BMCLE8; ISSN: 0960-894X
                         Elsevier Science B.V.
PUBLISHER:
                         Journal
DOCUMENT TYPE:
                         English
LANGUAGE:
    The expression of many staphylococcal virulence factors are regulated by
     the agr locus via a two-component signal transduction system
     (TCSTS), which is activated in response to a secreted autoinducer peptide
     (AIP). By exploiting the unique chemical architecture of the naturally
     occurring AIP-1, several potent inhibitors of staphylococcal TCSTS were
     designed and synthesized using either a linear or branched solid-phase
     approach. These prepared inhibitors I [R1 = CH(NH2)(S)-CH24-C6H4OH, R2 =
     Me, or CH2Me; R1 = (CH2)3OC6H4CH2Ph, or (CH2)3OC6H4COPh, R2 = Me] are
     competitive binders and contain the crucial 16-membered side-chain-to-tail
```

thiolactone peptide pharmacophore.

REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L76 ANSWER 14 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:

2003:171160 CAPLUS

DOCUMENT NUMBER:

138:332795

TITLE:

AUTHOR(S):

PUBLISHER:

Transcriptional induction of the penicillin-binding

protein 2 gene in Staphylococcus aureus by cell wall-active antibiotics oxacillin and vancomycin Boyle-Vavra, Susan; Yin, Shaohui; Challapalli,

Mamatha; Daum, Robert S.

CORPORATE SOURCE:

Department of Pediatrics, The University of Chicago,

Chicago, IL, 60637, USA

SOURCE:

Antimicrobial Agents and Chemotherapy (2003), 47(3),

1028-1036

CODEN: AMACCQ; ISSN: 0066-4804 American Society for Microbiology

DOCUMENT TYPE:

Journal English

LANGUAGE:

We found an increased abundance of pbpB-specific transcripts in vancomycin intermediate-resistant Staphylococcus aureus (VISA) isolates compared with that found in paired, genetically identical, susceptible isolates. This difference in expression cannot be explained by differences in the pbpB promoter sequence. Since the factors controlling pbpB gene expression have remained largely unexplored, various conditions that might affect VISA strains, pbpB expression varied with the growth phase, with the highest abundance of pbpB-specific transcripts detected during mid-log phase. Interestingly, both vancomycin and oxacillin were able to induce pbpB transcription above a constitutive level. When vancomycin was absent, one of the three pbpB-specific transcripts that were usually faintly detected in non-VISA strains was more readily detected in VISA strains during mid-log but not stationary phase. This transcript was enhanced in non-VISA strains by vancomycin induction. Gel shift assays indicated that an increased amount of the putative transcription factor that binds to both P1 and P1' promoter regions is present in the cytosol of vancomycin-induced cells. Neither the SigB sigma factor nor the quorum-sensing agr locus was required for growth phase-variable pbpB expression or transcriptional induction of pbpB by vancomycin or oxacillin. Also, MecI, MecRl, BlaI, and BlaRl, regulatory proteins that mediate β - lactam-inducible expression of mecA and β -lactamase, were not required for antibiotic induction of pbpB transcription. These data support the idea that pbpB expression is modulated by a trans-acting factor in response to the presence of the cell

REFERENCE COUNT:

51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L76 ANSWER 15 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:

2002:869046 CAPLUS

DOCUMENT NUMBER:

137:363038

wall-active antibiotics vancomycin and oxacillin.

TITLE:

Antimicrobial cyclic peptides, compositions containing

them, and screening methods

INVENTOR(S):

Ghadiri, M. Reza; Kim, Hui-Sun; Fernandez-Lopez, Sara;

Wilcoxen, Keith

PATENT ASSIGNEE(S):

The Scripps Research Institute, USA

SOURCE:

PCT Int. Appl., 240 pp. CODEN: PIXXD2

DOCUMENT TYPE:

Patent

LANGUAGE:

English

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FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:
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PATENT NO.
                            KIND DATE
                                                      APPLICATION NO. DATE
                           A2
      WO 2002090503
                                    20021114
                                                     WO 2002-US14329 20020506
           W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
                CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
                GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
                LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
                PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
                UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
                TJ, TM
           RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,
                BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
                                                      WO 2003-US14240 20030506
      WO 2003093300
                            A2
                                  20031113
               AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
                CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ,
                MD, RU, TJ, TM
           RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
                CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC,
                NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
                GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.:
                                                   US 2001-288990P P 20010504
                                                   WO 2002-US14329 A 20020506
```

The invention provides antimicrobial agents and compns. that include AR cyclic peptides having an amino sequence of alternating D-and $L-\alpha$ -amino acids. Alternatively, the cyclic peptides are made from β -amino acids. Methods for identifying and evaluating antimicrobial cyclic peptides are also provided.

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L76 ANSWER 16 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN
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ACCESSION NUMBER:

2002:676289 CAPLUS

DOCUMENT NUMBER:

137:211942

TITLE:

Drug design against drug resistant mutants using

directed evolution and target protein

conformation changes

INVENTOR(S):

Stevens, Raymond C.; Orencia, Maria C.; Yoon, Jun S.;

Hanson, Michael A.

PATENT ASSIGNEE(S):

The Scripps Research Institute, USA

SOURCE:

PCT Int. Appl., 82 pp. CODEN: PIXXD2

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO. DATE							
WO 200206893		20020906	WO 2002-US6238 20020227							
W: AE,	AG, AL, AM CR, CU, CZ	, AT, AU,								
•	HR, HU, ID		-							
	LT, LU, LV PT, RO, RU									

UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,

```
TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH,
              CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,
              BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.:
                                          US 2001-272248P P 20010228
     The present invention provides methods for identifying new drugs and
     potential inhibitors and modulators of drug-resistant variants of a target
     protein of a drug of interest. A drug-resistant variant according to the
     invention has at least one mutation resulting in a structural change, an
     activity change or a stability change as compared to the target protein.
     Such variants would include natural variants such as those encountered in
     the clinic, but preferably variants are selected by directed evolution
     methodol. The present invention relates to methods for designing new
     drugs useful against drug-resistant bacterial cells, viruses, mammalian
     cells and the like. The method involves identifying a target protein of the drug, selecting for drug-resistant variants that have an altered
     target protein (variant protein) by directed evolution, determining the three
     dimensional structure of the target and variant proteins and designing a
     new drug that can be effective against at least one drug-resistant
     variant. The present invention can be used to predict future mutations
     that lead to drug resistance and the type of drugs that are effective to
     combat such resistance.
L76 ANSWER 17 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:
                          2002:71893 CAPLUS
DOCUMENT NUMBER:
                          136:129034
TITLE:
                          Antimicrobial sulfonamide derivatives of lipopeptide
                          antibiotics
INVENTOR(S):
                          Curran, William V.; Leese, Richard A.; Jarolmen,
                          Howard; Borders, Donald B.
                          Intrabiotics Pharmaceuticals, Inc., USA
PATENT ASSIGNEE(S):
                          PCT Int. Appl., 67 pp.
SOURCE:
                          CODEN: PIXXD2
DOCUMENT TYPE:
                          Patent
LANGUAGE:
                          English
FAMILY ACC. NUM. COUNT:
PATENT INFORMATION:
     PATENT NO.
                     KIND DATE
                                            APPLICATION NO. DATE
                             ----
     ----
                                            _____
                                           WO 2001-US22352 20010717
     WO 2002005837
                      A1 20020124
         W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
             LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO,
             RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN,
             YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
             DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
             BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
                                        EP 2001-957162 20010717
                      A1 20030521
             AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRIORITY APPLN. INFO.:
                                          US 2000-219059P P 20000717
                                          US 2000-220950P P 20000726
                                          US 2001-760328
                                                           A 20010112
                                          WO 2001-US22352 W 20010717
OTHER SOURCE(S):
                          MARPAT 136:129034
    The invention provides antimicrobial sulfonamide derivs. of lipopeptide
```

antibiotics, pharmaceutical compns. of antimicrobial sulfonamide derivs.,

Mitra 10/032,950

methods for making antimicrobial sulfonamide derivs., methods for inhibiting microbial growth with antimicrobial sulfonamide derivs., and methods for treating or preventing microbial infections in a subject with antimicrobial sulfonamide derivs. Antimicrobial sulfonamide derivs. are generally an amino core antibiotic that has been further modified with a lipophilic sulfonyl group.

REFERENCE COUNT:

THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L76 ANSWER 18 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:

2002:907161 CAPLUS

DOCUMENT NUMBER:

138:13500

TITLE:

Superantigen-glycolipid conjugates loaded onto antigen

presening cells for adoptive immunotherapy of

neoplastic and infectious diseases

INVENTOR(S):

Terman, David S.

PATENT ASSIGNEE(S):

USA

SOURCE:

U.S. Pat. Appl. Publ., 167 pp.

CODEN: USXXCO

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE _____ US 2001-870759 20010530 A1 US 2002177551 20021128 US 2000-208128P P 20000531 PRIORITY APPLN. INFO.:

The present invention comprises compns. and methods for treating a tumor or neoplastic disease in a host, The methods employ conjugates comprising superantigen polypeptides, nucleic acids with other structures that preferentially bind to tumor cells and are capable of inducing apoptosis. Also provided are superantigen-glycolipid conjugates and vesicles that are loaded onto antigen presenting cells to activate both T cells and NKT cells. Cell-based vaccines comprise tumor cells engineered to express a superantigen along with glycolipids products which, when expressed, render the cells capable of eliciting an effective anti-tumor immune response in a mammal into which these cells are introduced. Included among these compns. are tumor cells, hybrid cells of tumor cells and accessory cells, preferably dendritic cells. Also provided are tumoricidal T cells and NKT cells devoid of inhibitory receptors or inhibitory signaling motifs which are hyperresponsive to the the above compns. and lipid-based tumor associated antigens that can be administered for adoptive immunotherapy of cancer and infectious diseases.

L76 ANSWER 19 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:

2002:874013 CAPLUS

DOCUMENT NUMBER:

138:106988

TITLE:

Synthesis of Novel Nocathiacin-Class Antibiotics. Condensation of Glycolaldehyde with Primary Amides and

Tandem Reductive Amination of Amadori-Rearranged

2-Oxoethyl Intermediates.

AUTHOR(S):

Hrnciar, Peter; Ueda, Yasutsugu; Huang, Stella; Leet,

John E.; Bronson, Joanne J.

CORPORATE SOURCE:

Pharmaceutical Research Institute, Bristol-Myers

Squibb Co., Wallingford, CT, 06492, USA

SOURCE:

Journal of Organic Chemistry (2002), 67(25), 8789-8793

CODEN: JOCEAH; ISSN: 0022-3263

PUBLISHER:

American Chemical Society

DOCUMENT TYPE:

Journal

LANGUAGE:

English

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OTHER SOURCE(S):
                         CASREACT 138:106988
    Nocathiacin I, I [R = NHC(:CH2)CONH2], and nocathiacin IV, I (R = NH2),
     are novel indole-containing thiazolyl cyclic peptide antibiotics, which
     exhibit potent activity against key Gram-pos. bacterial pathogens,
     including multi drug-resistant Staphylococcus aureus, Streptococcus
     pneumoniae, and Enterococcus faecium. New nocathiacins I (R =
     NHCH2CH2NR1R2; NR1R2 = morpholine; R1 = R2 = CH2CH2OH; R1 = Et, R2 =
     CH2CH2OH; R1 = Me, R2 = CH2CH2OH; R1 = R2 = Et; R1 = Et, R2 = CH2CO2H)
     were prepared from nocathiacin IV by condensation with glycolaldehyde dimer
     followed by tandem reductive amination of the intermediate with NHR1R2.
     This transformation readily tolerated the complex architecture of
     nocathiacin IV and allowed selective incorporation of water-solubilizing
     groups to the primary amide in nocathiacin IV without needing the presence
     of protecting groups.
REFERENCE COUNT:
                               THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS
                               RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
L76 ANSWER 20 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:
                         2002:853427 CAPLUS
DOCUMENT NUMBER:
                         138:304509
TITLE:
                         The synthesis of a novel binaphthyl-based cyclic
                         peptoid with anti-bacterial activity
                         Bremner, John B.; Coates, Jonathan A.; Coghlan, Daniel
AUTHOR(S):
                         R.; David, Dorothy M.; Keller, Paul A.; Pyne, Stephen
                         Department of Chemistry, University of Wollongong,
CORPORATE SOURCE:
                         Wollongong, 2522, Australia
                         New Journal of Chemistry (2002), 26(11), 1549-1551
SOURCE:
                         CODEN: NJCHE5; ISSN: 1144-0546
PUBLISHER:
                         Royal Society of Chemistry
DOCUMENT TYPE:
                         Journal
LANGUAGE:
                         English
OTHER SOURCE(S):
                         CASREACT 138:304509
     The novel cyclic peptoid I, based upon a 1,1'-binaphthyl scaffold and a
     bridging tripeptide moiety, was synthesized utilizing a ring-closing
     metathesis reaction. The individual major and minor diastereomers of
     compound I were shown to have promising anti-bacterial activity against
     Staphylococcus aureus with inhibition of microbial growth at 17 \muL-1m
     (MIC) and 31 \mug ml-1, resp.
REFERENCE COUNT:
                         25
                               THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS
                               RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
L76 ANSWER 21 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:
                         2002:287801 CAPLUS
                         137:185805
DOCUMENT NUMBER:
TITLE:
                         Synthesis and evaluation of vancomycin and vancomycin
                         aglycon analogues that bear modifications in the
                         residue 3 asparagine
                         McAtee, J. Jeffrey; Castle, Steven L.; Jin, Qing;
AUTHOR(S):
                         Boger, Dale L.
                         Department of Chemistry and The Skaggs Institute for
CORPORATE SOURCE:
                         Chemical Biology, The Scripps Research Institute, La
                         Jolla, CA, 92037, USA
SOURCE:
                         Bioorganic & Medicinal Chemistry Letters (2002),
                         12(9), 1319-1322
                         CODEN: BMCLE8; ISSN: 0960-894X
PUBLISHER:
                         Elsevier Science Ltd.
DOCUMENT TYPE:
                         Journal
LANGUAGE:
                         English
                         CASREACT 137:185805
OTHER SOURCE(S):
```

The synthesis and biol. evaluation of a set of residue 3 analogs of

vancomycin and its aglycon are described. These investigations follow from the promising biol. activity of a protected and synthetically modified vancomycin aglycon analog in which the asparagine side chain was modified to possess a nitrile, rather than a carboxamide. Although this modification typically was detrimental to antimicrobial activity, hydrophobic vancomycin aglycon analogs that lack a lipid anchor as well as the disaccharide are detailed that exhibit unusual potency against VanB, but not VanA, resistant bacteria.

REFERENCE COUNT:

THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L76 ANSWER 22 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:

2001:152655 CAPLUS

DOCUMENT NUMBER:

134:193744

TITLE:

Preparation of macrocyclic compounds for treating

bacterial infections

INVENTOR(S):

Jefferson, Elizabeth; Swayze, Eric Edward

Isis Pharmaceuticals, Inc., USA

SOURCE:

PCT Int. Appl., 98 pp. CODEN: PIXXD2

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT ASSIGNEE(S):

```
APPLICATION NO.
                      KIND DATE
     PATENT NO.
                                             WO 2000-US22871 20000818
                             20010301
     WO 2001014346
                      A1
         W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
             HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
             LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
             SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
             YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
             DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
                                            US 1999-378529 19990820
                             20031209
     US 6660832
                       В1
                                          US 1999-378529
                                                           A 19990820
PRIORITY APPLN. INFO.:
                          MARPAT 134:193744
OTHER SOURCE(S):
     Macrocyclic compds. I [X = O, NH, S; R1-R4 = H, amino or an amino acid
```

AB Macrocyclic compds. I [X = O, NH, S; R1-R4 = H, amino or an amino acid side chain; R5 = H, OH, CO2H, halo, SH, cyano, amino, an electron withdrawing group, alkoxy, C(O)NH2, -C(O)NHR6, C(O)-(amino acid)1-4, -C(O)OR6, CH2OH, -CH2OR6, NHC(O)R7, or -NH-(amino acid)1-4; R6, R7 = alkyl (optionally substituted with OH, halogen, CO2H, cyano, amino, amidine, guanidine, urea, or a nucleobase) or aryl, aralkyl, heterocyclyl, or heterocyclyalkyl optionally substituted with OH, halogen, CO2H, oxo, cyano, amino, amidine, guanidine, or urea (the substituent may also be C1-4 alkyl in the case of R7)] are useful for therapeutic and prophylactic treatment of bacterial infection in mammals. Solid phase synthetic procedures are given for the synthesis of a library of macrocyclic compds. using KanTM reactors. Claimed compds. include macrocycle II. Min. inhibitory concentration and coupled bacterial transcription/translation data are tabulated.

L76 ANSWER 23 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:

2001:225071 CAPLUS

DOCUMENT NUMBER:

135:16454

TITLE:

Pseudodestruxins A and B: New Cyclic Depsipeptides from the Coprophilous Fungus Nigrosabulum globosum Che, Yongsheng; Swenson, Dale C.; Gloer, James B.;

AUTHOR(S):

Koster, Brenda; Malloch, David

CORPORATE SOURCE: Department of Chemistry, University of Iowa, Iowa

City, IA, 52242, USA

SOURCE: Journal of Natural Products (2001), 64(5), 555-558

CODEN: JNPRDF; ISSN: 0163-3864

PUBLISHER: American Chemical Society

DOCUMENT TYPE: Journal LANGUAGE: English

AB Pseudodestruxins A (I) and B (II), two new cyclic peptides, have been isolated from cultures of the coprophilous fungus Nigrosabulum globosum. The structure of pseudodestruxin A was elucidated using 2D NMR techniques and confirmed by single-crystal X-ray diffraction anal. The structure of pseudodestruxin B was assigned by comparing its NMR and FABMS data with those of pseudodestruxin A. The known compds. ascochlorin and 5-chlorocollectorin B were also isolated from N. globosum. Although Pseudodestruxins A and B display antibacterial effects, ascochlorin was found to be responsible for the antifungal activity of the crude extract

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L76 ANSWER 24 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1999:297439 CAPLUS

DOCUMENT NUMBER: 130:297010

TITLE: Preparation of cyclic peptides having broad spectrum

antimicrobial activity

INVENTOR(S): Chang, Conway; Gu, Leo; Chen, Jie

PATENT ASSIGNEE(S): Intrabiotics Pharmaceuticals, Inc., USA

SOURCE: PCT Int. Appl., 167 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

LANGUAGE:

PE: Patent English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO. KIND DAT									A1	PPLI	CATI	ON NO	o.	DATE			
WO	9921	879		Α	1	1999	0506	WO 1997-US19557 19971027									
	W:	AL,	ΑM,	ΑU,	ΑZ,	BA,	BB,	ВĠ,	BR,	BY,	CA,	CN,	CU,	CZ,	EE,	GΕ,	GH,
		HU,	ID,	ΙL,	IS,	JΡ,	KG,	KΡ,	KR,	ΚZ,	LC,	LK,	LR,	LT,	LV,	MD,	MG,
		MK,	MN,	MX,	NO,	NΖ,	PL,	RO,	RU,	SG,	SI,	SK,	SL,	ТJ,	TM,	TR,	TT,
		UA,	UZ,	VN,	YU,	AM,	ΑZ,	BY,	KG,	KΖ,	MD,	RU,	ТJ,	TM			
	RW:	GH,	ΚE,	LS,	MW,	SD,	SZ,	UG,	ZW,	AT,	BE,	CH,	DE,	DK,	ES,	FΙ,	FR,
		GB,	GR,	ΙE,	ΙT,	LU,	MC,	NL,	PT,	SE,	BF,	ΒĴ,	CF,	CG,	CI,	CM,	GΑ,
		GN,	ML,	MR,	ΝE,	SN,	TD,	ΤG									
AU 9851535 A1 19990517 AU 1998-5											98-5	1535		1997	1027		
D T m t	7 7 7 7 7	T N.T	TMEO	_				1	M 1 €	207	rrc1 0	557		1007	1027		

PRIORITY APPLN. INFO.: WO 1997-US19557 The present invention provides cyclic peptides I [m = 0-2, n = 0-1, withthe proviso that when m = 2, n = 0; X21, X22, X24, X25, X27, X28 are each independently present or absent; X7 and X4 are either both present or both absent; X8 and X3 are either both present or both absent; X2-X5, X7, X8, X13, X14, X16-X19, X21, X22, X27, X28 independently = hydrophobic amino acid, hydrophilic amino acid, small amino acid, with provisos (i) when X2 = hydrophobic amino acid, X7, X14, X19, X21, and X28 independently = hydrophobic amino acid or small amino acid and X3, X8, X13, X18, X22 and X27 independently = hydrophilic amino acid or small amino acid and (ii) when X2 = hydrophilic amino acid X7, X14, X19, X21, and X28 independently = hydrophilic amino acid or small amino acid and X3, X8, X13, X18, X22 and X27 independently = hydrophobic amino acid or small amino acid; X23-X26 taken together = loop; Z1, Z6, Z5, Z20 independently = hydrophilic amino acid, small amino acid, cysteine-like amino acid; X9-X12 taken together = β -turn; at least one of X9-X12, X23-X26 = basic amino acid; and

wherein the peptide has net pos. charge at physiol. pH] comprising and amphiphilic antiparallel β -sheet region, a loop region, and a β -turn region having broad spectrum antimicrobial activity. The peptides exhibit improved efficacy, bioavailability and/or serum half-life as compared with non-cyclized analogs. Thus, cystine-containing cyclopeptide II inhibited Pseudomonas aeruginosa with MIC = $8 \mu g/mL$ and methicillin-resistant Staphylococcus aureus with $\dot{\text{MIC}}$ = 2 $\mu\text{g/mL}$ compared to 32 μ g/mL against both bacteria for the uncyclized peptide. In addition, II showed increased activities after 15 min and 120 min relative to the uncyclized peptide.

REFERENCE COUNT:

THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L76 ANSWER 25 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN

1

ACCESSION NUMBER:

1998:719131 CAPLUS

DOCUMENT NUMBER: TITLE:

130:4085 Preparation of peptides with bactericidal activity and

endotoxin neutralizing activity for gram negative

INVENTOR(S):

Gray, Beulah H.; Haseman, Judith R.; Mayo, Kevin H.

PATENT ASSIGNEE(S):

Regents of the University of Minnesota, USA

SOURCE:

U.S., 56 pp., Cont.-in-part of U.S. Ser. No. 218,026.

CODEN: USXXAM

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PA.	TENT NO.	KIND	DATE	APPLICATION NO. DATE
		A	19981103	US 1996-653632 19960524 US 1994-218026 19940324
	5786324	A	19980728	1007050
WO	9744354		19971127	WO 1997-050944 19970525
	W: CA, JP, RW: AT, BE,	CH, DE	, DK, ES,	FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
EP	939766		19990908	EP 1997-928665 19970523
.TP	R: DE, FR, 2000511892		, SE 20000912	JP 1997-542843 19970523
			20021126	
US	2003153502	A1	20030814	US 2002-300083 20021120
PRIORIT	Y APPLN. INFO	.:		US 1994-218026 A2 19940324 US 1996-653632 A2 19960524
				US 1996-671487 A2 19960627
				WO 1997-US8944 W 19970523
•				US 1999-194296 A3 19991015

The invention provides biol. active peptides derived from or corresponding AB to regions of a bactericidal permeability increasing factor (B/PI). The peptides are preferably about 10 to 100 amino acids long and have bactericidal and/or endotoxin neutralizing activity. The peptides can be prepared by automated protein synthesis or by recombinant DNA methods. The peptides are useful in methods to treat and prevent bacterial infection in the body and on surfaces. The peptides are also useful to treat endotoxin shock and have endotoxin neutralizing activity.

REFERENCE COUNT: 35

THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L76 ANSWER 26 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:

1998:508906 CAPLUS

DOCUMENT NUMBER:

129:156917

TITLE:

Synthetic peptides with bactericidal activity and endotoxin neutralizing activity for gram negative bacteria and methods for their use

INVENTOR(S): Gray, Beulah; Haseman, Judith R.; Mayo, Kevin

PATENT ASSIGNEE(S): Regents of the University of Minnesota, USA

SOURCE: U.S., 46 pp.
CODEN: USXXAM

DOCUMENT TYPE: Patent

LANGUAGE: English FAMILY ACC. NUM. COUNT: 4

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5786324	А	19980728	US 1994-218026	19940324
US 5830860	Α	19981103	US 1996-653632	19960524
PRIORITY APPLN.	INFO.:		US 1994-218026 A2	19940324

AB The invention provides biol. active peptides derived from or corresponding to regions of a bactericidal permeability increasing factor (B/PI). The peptides are about 10 to 100 amino acids long and have bactericidal and/or endotoxin neutralizing activity. The peptides can be prepared by automated DNA synthesis or by recombinant DNA methods. The peptides are useful in methods to treat and prevent bacterial infection in the body and on surfaces. The peptides are also useful to treat endotoxin shock.

REFERENCE COUNT: 76 THERE ARE 76 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L76 ANSWER 27 OF 34 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1997:414155 CAPLUS

DOCUMENT NUMBER: 127:31334

TITLE: Kawaquchipeptin B, an antibacterial cyclic

undecapeptide from the cyanobacterium Microcystis

aeruginosa

AUTHOR(S): Ishida, Keishi; Matsuda, Hisashi; Murakami, Masahiro;

Yamaguchi, Katsumi

CORPORATE SOURCE: Laboratory of Marine Biochemistry Graduate School of

Agricultural Life Sciences, University of Tokyo,

Tokyo, 113, Japan

SOURCE: Journal of Natural Products (1997), 60(7), 724-726

CODEN: JNPRDF; ISSN: 0163-3864

PUBLISHER: American Chemical Society

DOCUMENT TYPE: Journal LANGUAGE: English

AB Kawaguchipeptin B, an antibacterial cyclic undecapeptide, was isolated from the cultured cyanobacterium Microcystis aeruginosa (NIES-88). Its structure was elucidated as (I) on the basis of 2D NMR data and chemical degradation I inhibited the growth of the Gram-pos. bacterium Staphylococcus aureus at a concentration of 1 μ g/mL (MIC).

L76 ANSWER 28 OF 34 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: DOCUMENT NUMBER:

2004:22398 BIOSIS PREV200400009801

TITLE:

An engineered multidomain bactericidal

peptide as a model for targeted antibiotics against

specific bacteria.

AUTHOR(S): Qiu, Xiao-Qing; Wang, He; Lu, Xiao-Fong; Zhang, Jie; Li,

Sheng-Fu; Cheng, Gang; Wan, Lin; Yang, Li; Zuo, Jun-Yong; Zhou, Yu-Qi; Wang, Hai-Yun; Cheng, Xin; Zhang, Su-Hua; Ou, Zheng-Rong; Zhong, Zi-Cheng; Cheng, Jing-Qiu; Li, You-Ping;

Wu, George Y. [Reprint Author]

CORPORATE SOURCE: Division of Gastroenterology-Hepatology, University of

Connecticut Health Center, Farmington, CT, 06030-1845, USA

qiu@mrsa.com.cn; wu@nso.uchc.edu

SOURCE:

Nature Biotechnology, (December 2003) Vol. 21, No. 12, pp.

1480-1485. print.

ISSN: 1087-0156 (ISSN print).

DOCUMENT TYPE:

Article English

LANGUAGE: OTHER SOURCE:

DDBJ-AF001782; EMBL-AF001782; GenBank-AF001782; DDBJ-AF001783; EMBL-AF001783; GenBank-AF001783;

DDBJ-U85097; EMBL-U85097; GenBank-U85097

ENTRY DATE:

Entered STN: 24 Dec 2003

Last Updated on STN: 24 Dec 2003

We constructed a peptide consisting of a staphylococcal AgrDl pheromone AB fused to the channel-forming domain of colicin la and named it pheromonicin. This fusion peptide had bactericidal effects against methicillin-sensitive and methicillin-resistant Staphylococcus aureus (MSSA and MRSA, respectively), but not against Staphylococcus epidermidis or Streptococcus pneumoniae.

Growth rates, vital staining and colony forming unit (CFU) counts showed that pheromonicin did not merely suppress growth but killed S. aureus cells. The specificity of pheromonicin was shown by the

absence of bactericidal effects against an accessory

gene regulator (agr) locus knockout of

S. aureus, and a dose-dependent inhibition of the bactericidal effects of pheromonicin by competition with

corresponding free AgrD pheromone. In vivo, all pheromonicin-treated mice survived administration of MRSA that was lethal to controls. No toxicity was detectable in human liver or renal cells in culture, or in livers, kidneys or spleens of pheromonicin-treated mice. The results suggest that these types of chimeric peptides may be of value as antibiotics against specific bacterial infections.

L76 ANSWER 29 OF 34 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

ACCESSION NUMBER:

2003-606005 [57] WPIDS

CROSS REFERENCE:

1996-209319 [21]; 1998-018426 [02]; 2003-074097 [07]

DOC. NO. CPI:

C2003-165005

TITLE:

New purified peptide that inhibits agr-rnaIII

transcription in Staphylococcus aureus

, useful for treating or preventing a staphylococcal

infection or disease.

DERWENT CLASS:

B04 INVENTOR(S):

BEAVIS, R; JI, G; NOVICK, R P

PATENT ASSIGNEE(S):

(BEAV-I) BEAVIS R; (JIGG-I) JI G; (NOVI-I) NOVICK R P

COUNTRY COUNT:

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG _____ US 2003078378 A1 20030424 (200357)* 12

APPLICATION DETAILS:

PATENT NO KIND		APPLICATION	DATE
US 2003078378 A1	CIP of CIP of Cont of	US 1994-318499 US 1996-651226 US 1997-861476 US 2002-201444	19941004 19960522 19970522 20020723

FILING DETAILS:

PATENT	NO	KIND	PATENT	NO

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US 2003078378 Al Cont of
```

US 6447786

PRIORITY APPLN. INFO: US 1997-861476 19970522; US 1994-318499 19941004; US 1996-651226 19960522; US

2002-201444 20020723

AB US2003078378 A UPAB: 20030906

NOVELTY - A purified peptide, which inhibits agr-rnaIII transcription in Staphylococcus aureus, is new. The peptide contains 6-12 amino acids in length and comprises amino acid 28 from the AgrD region of a Staphylococcibacterium, or its analogue.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

- (1) a peptide composition comprising the purified peptide cited above and a pharmaceutical carrier; and
- (2) treating or preventing an infection or disease caused by **S. aureus** in a subject comprising administering to the subject the purified peptide.

ACTIVITY - Antibacterial.

No biological data given.

MECHANISM OF ACTION - Virulence Factor Inhibitor.

USE - The purified peptides and compositions are useful for treating or preventing an infection or disease caused by a Staphylococci bacterium. ${\rm Dwg.0/4}$

L76 ANSWER 30 OF 34 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

ACCESSION NUMBER:

2002-681366 [73] WPIDS

CROSS REFERENCE:

2002-170774 [22]

DOC. NO. CPI:

C2002-192257

TITLE:

New cyclic peptides, useful for treating Staphylococcus aureus

infections.

DERWENT CLASS:

A96 B04

INVENTOR(S):

BEAVIS, R; JI, G; MAYVILLE, P; MUIR, T W; NOVICK, R P (BEAV-I) BEAVIS R; (JIGG-I) JI G; (MAYV-I) MAYVILLE P;

PATENT ASSIGNEE(S):

(MUIR-I) MUIR T W; (NOVI-I) NOVICK R P

COUNTRY COUNT:

PATENT INFORMATION:

PATI	ENT	NO	KIND	DATE	WEEK	LA	PG
IIS '	2002	07745	3 A1	20020620	(200273)*		18

APPLICATION DETAILS:

PATE	ENT NO	KIND		API	PLICATION	DATE
US 2	20020774		Provisional Cont of	US	1998-90402P 1999-339511 2001-32950	19980624 19990624 20011227

PRIORITY APPLN. INFO: US 1998-90402P 19980624; US 1999-339511 19990624; US 2001-32950 20011227

AB US2002077453 A UPAB: 20021113

NOVELTY - A cyclic peptide is new.

DETAILED DESCRIPTION - A cyclic peptide of

formula (I) is new.

X = amino acid, amino acid analog, peptidomimetic or non-amide isostere;

Z' = synthetic or biosynthetic amino acid;

R = O, N or C;

n = 0-10; and

```
v = 1-10.
          INDEPENDENT CLAIMS are included for:
          (1) a cyclic peptide of formula H2N-Xn-Z'-Xy-COOH
     (II) with a cyclic bond between Z' and COOH other than a thioester bond;
          (2) compositions comprising the peptides;
          (3) method for treating S. aureus infection
     comprises administration of the composition;
          (4) method for preparing (I).
          ACTIVITY - Antibacterial.
         MECHANISM OF ACTION - Agr response inhibitor.
          USE - The peptides are useful for treating S.
     aureus infections (claimed).
     Dwq.0/3
L76 ANSWER 31 OF 34 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
                     2002-170774 [22]
                                       WPIDS
ACCESSION NUMBER:
                      2002-681366 [73]
CROSS REFERENCE:
                     C2002-052666
DOC. NO. CPI:
                      Novel synthetic, cyclic AgrD-autoinducing
TITLE:
                      peptide for bacterial interference and for
                      treating Staphylococcus aureus
                      infection in a subject.
DERWENT CLASS:
                      B03 B04 D16
                      BEAVIS, R; JI, G; MAYVILLE, P; MUIR, T W; NOVICK, R P
INVENTOR(S):
                      (UYNY) UNIV NEW YORK STATE; (UYRQ) UNIV ROCKEFELLER
PATENT ASSIGNEE(S):
COUNTRY COUNT:
                      1
PATENT INFORMATION:
                KIND DATE
     PATENT NO
                 -------
                 B1 20020108 (200222)*
    US 6337385
APPLICATION DETAILS:
                                                        DATE
                                       APPLICATION
     PATENT NO KIND
                                       US 1998-90402P
                                                        19980624
     US 6337385 B1 Provisional
                                       US 1999-339511
                                                        19990624
PRIORITY APPLN. INFO: US 1998-90402P
                                      19980624; US 1999-339511
                      19990624
     US 6337385 B UPAB: 20021118
     NOVELTY - A synthetic cyclic peptide (I), in
     particular a AgrD-autoinducing peptide, where AgrD is a secreted
     agr-encoded peptide, where the agr locus controls the
     synthesis of virulence factor and other extracellular proteins responsible
     for pathogenicity in Staphylococcus aureus, is new.
          DETAILED DESCRIPTION - A synthetic cyclic peptide
     (I) with formula (A) or NH2-X(n)-Z-X(y)-\overline{COOH}, and a cyclic bond between Z
     residue and COOH other than a thioester bond, in particular a
     AgrD-autoinducing peptide, where AgrD is a secreted agr-encoded
     peptide, where the agr locus controls the synthesis of virulence
     factor and other extracellular proteins responsible for pathogenicity in
     Staphylococcus aureus, is new.
          X = an amino acid, its analog, peptidomimetic, or nonamide isostere;
          Z' = synthetic or biosynthetic amino acid;
          R = oxygen, nitrogen, sulfur or carbon;
     n = 0-10; or
     y = 1-10.
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AΒ

INDEPENDENT CLAIMS are also included for the following:

(1) a pharmaceutical composition (II) comprising (I), and a carrier; and

(2) preparing (I).

ACTIVITY - Antibacterial.

MECHANISM OF ACTION - Inhibitor of Agr response. Synthetic approach was used to prepare AgrD peptides from Staphylococcus aureus group I and group II strains. The biological activity of the synthetic AgrD peptides was assayed using cultured ${\bf S}$. aureus strains containing a beta -lactamase reporter gene fused to agrP3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically using a calorimetric beta -lactamase activity assay. As with their naturally derived counterparts, synthetic AgrD peptide was found to activate the agr response only within their own S. aureus class, and inhibit the agr response only in S. aureus strains from the other two classes.

USE - (I) is useful for bacterial interference, especially for treating S. aureus infection in a subject. Dwg.0/3

L76 ANSWER 32 OF 34 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

ACCESSION NUMBER:

2000-147202 [13] WPIDS

DOC. NO. CPI:

C2000-046059

TITLE:

New cyclic peptides for treating

infections with Staphylococcus aureus

DERWENT CLASS:

A96 B04

87

INVENTOR(S): PATENT ASSIGNEE(S): BEAVIS, R; JI, G; MAYVILLE, P; MUIR, T W; NOVICK, R P (UYNY) UNIV NEW YORK STATE; (UYRQ) UNIV ROCKEFELLER

COUNTRY COUNT:

PATENT INFORMATION:

WEEK PATENT NO KIND DATE _____

WO 9967286 A2 19991229 (200013)* EN 36

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL

OA PT SD SE SL SZ UG ZW

W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR

TT UA UG US UZ VN YU ZA ZW

A 20000110 (200025) AU 9947238

A2 20010411 (200121) EN EP 1090034

R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE

JP 2002519304 W 20020702 (200246)

APPLICATION DETAILS:

PATENT NO K	IND	AP	PLICATION	DATE
WO 9967286 AU 9947238 EP 1090034 JP 2002519304	A2 A A2 W	AU EP WO WO	1999-US14562 1999-47238 1999-930780 1999-US14562 1999-US14562 2000-555937	19990624 19990624 19990624 19990624 19990624
		UΞ	2000 55555	1000021

FILING DETAILS:

PATENT NO KIND PATENT NO AU 9947238 A Based on WO 9967286 EP 1090034 A2 Based on WO 9967286 JP 2002519304 W Based on WO 9967286

PRIORITY APPLN. INFO: US 1998-103438 19980624

AB WO 9967286 A UPAB: 20000313

NOVELTY - Cyclic peptides (I) derived from AgrD peptides of Staphylococcus aureus are new.

DETAILED DESCRIPTION - (I) are:

(i) of formula (Ia), or

(ii) (Ib), comprise the sequence NH2-Xn-Z-Xy-COOH with a cyclic bond, other than thioester, between Z and COOH:

 $X = amino \ acid \ (aa)$, aa analog, peptidomimetic or non-amide isostere;

Z = synthetic or natural aa;

R = oxygen, nitrogen or carbon;

n = 0-10;v = 1-10

INDEPENDENT CLAIMS are also included for the following:

(a) composition containing (I) and a carrier; and

(b) method for production of (I).

ACTIVITY - Antibacterial.

MECHANISM OF ACTION - (I) inhibits the agr response (associated with release of virulence factors) of S. aureus. Normally an AgrD peptide is produced by S. aureus that (i) activates the agr response in strains of a single group but (ii) interferes with this response in strains of different groups.

USE - (I) are used to treat infections by S. aureus

ADVANTAGE - (I), which mimic the AgrD peptides but have the thiololactone bond replaced by a different cyclic bond, lack the agr-inducing activity of the native peptide for specific bacterial strains, but retains the inhibitory activity against other strains. (I) can be produced in excellent yield by selective intermolecular cyclization/cleavage reaction of the resin-bound, unprotected, linear analog.

Dwg.0/3

L76 ANSWER 33 OF 34 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

ACCESSION NUMBER:

1999-370885 [31] WPIDS

DOC. NO. CPI:

C1999-109456

TITLE:

Cyclic antibacterial peptides

for treating and preventing bacterial infection in humans

and animals.

DERWENT CLASS:

B04 B07 C03 D22

INVENTOR(S):

AFFAS, Z M; BYCROFT, B W; CHAN, W C; MCDOWELL, P W;

STEWART, G S A B; WILLIAMS, P

PATENT ASSIGNEE(S):

(UYNO-N) UNIV NOTTINGHAM

COUNTRY COUNT:

83

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 9926968 A1 19990603 (199931)* EN 32

'RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZŴ

A 19990615 (199944) AU 9912490

APPLICATION DETAILS:

PAT	TENT NO	KIND	APPLICATION	DATE
WO	9926968	A1	WO 1998-GB3497	19981124
ΑU	9912490	A	AU 1999-12490	19981124

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9912490	A Based on	WO 9926968

PRIORITY APPLN. INFO: GB 1997-24859 19971126

WO 9926968 A UPAB: 20000516

NOVELTY - Cyclic peptides (I), their acid or base addition salts and prodrugs are new.

DETAILED DESCRIPTION - (I) have the formula:

A, B, E and D = residues of natural or synthetic amino acids (aa), optionally substituted;

m = 0-5;

= 1-5; ;

X = sulfur, oxygen or NR3;

R1, R2 and R3 = hydrogen, 1-6C alkyl, acyl or alkoxycarbonyl, or,

where m = 0, R1 and R2 may complete a heterocyclic ring;

each Z = residue as defined for A;

the peptide bonds in (I) are optionally substituted on nitrogen by 1-6C alkyl.

When n = 1, X = sulfur, and R1 = R2 = hydrogen and when:

- (i) ABED = Asp-Phe-Ile-Met respectively, (Z)m is not H-Tyr-Ser-Thr;
- (ii) ABED = Asn-Ala-Tyr-Phe respectively, (Z)m is not H-Asp-Ile;
- (iii) ABED = Asp-Phe-Leu-Leu respectively, (Z)m is not H-Tyr-Ile-Asn;
- (iv) ABED = Ser-Ser-Leu-Phe respectively, (Z)m is not H-Gly-Val-Asn-Ala.

INDEPENDENT CLAIMS are included for the following:

- (1) articles coated and/or impregnated with (I); and
- (2) compounds of formula (II):

where:

- (i) AlBlElD1 = Asp-Phe-Ile-Met respectively, Y is H-Tyr-Ser-Thr;
- (ii) A1B1E1D1 = Asn-Ala-Tyr-Phe respectively, Y is H-Asp-Ile;
- (iii) AlB1E1D1 = Asp-Phe-Leu-Leu respectively, Y is H-Tyr-Ile-Asn; or (iv) AlB1E1D1 = Ser-Ser-Leu-Phe respectively, Y is H-Gly-Val-Asn-Ala. ACTIVITY - Antibacterial.

MECHANISM OF ACTION - (I) are modulators of the agr response; agonists of this response antagonize early stages of virulence, specifically production of cell wall proteins (so are preferred for prophylaxis), while antagonists interfere with the later stages of virulence, specifically secretion of exotoxin (so are preferred for treatment). Staphylococcus aureus KH1187A was grown in nutrient broth containing 1.92 mu g/ml of the peptide ZA78, cyclo(Ac-Cys-Asp-Phe-Ile-Met), then the culture supernatant analyzed by electrophoresis and staining with Coomassie Blue. The band for toxic shock syndrome toxin-1, clearly visible in a control culture grown in absence of ZA78, was not detectable.

USE - (I) and (II) are used to treat or prevent bacterial infections in humans and animals, also for incorporation into medical articles, e.g tampons (to prevent toxic shock syndrome), prostheses and wound dressings. Particularly they are active against staphylococci, specifically

Staphylococcus aureus but also coagulase-negative S.

epidermidis, implicated in infection of medical implants.

ADVANTAGE - Some (I) are active against many different bacterial

strains. Dwg.0/0

L76 ANSWER 34 OF 34 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

LA

ACCESSION NUMBER:

1997-225834 [20] WPIDS

DOC. NO. CPI:

C1997-072303

TITLE:

Treatment of bacterial infections in mammals - by administering an inhibitor of a global regulator of

pathogenesis genes.

DERWENT CLASS:

B05

INVENTOR(S):

BAO, Y; BOGGS, A; CONTAG, P R; FEDERSPIEL, N A; HEBERT,

A; HECKER, S; MALOUIN, F

WEEK

PATENT ASSIGNEE(S):

(MICR-N) MICROCIDE PHARM INC

COUNTRY COUNT:

25

PATENT INFORMATION:

1	
1	1

PATENT NO KIND DATE

WO 9711690 A2 19970403 (199720)* EN 138

RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE

W: AU CA CU DE IL JP MX NZ

AU 9671686 A 19970417 (199732)

A3 19970912 (199749) WO 9711690

A 20000201 (200013) US 6020121

APPLICATION DETAILS:

PAT	CENT NO	KIND		API	PLICATION	DATE
AU WO	9711690 9671686 9711690 6020121	A2 A A3 A	Provisional	AU WO US	1996-US15435 1996-71686 1996-US15435 1995-4626P 1996-672215	19960925 19960925 19960925 19950929 19960625
				0.5	1770 012213	100002

FILING DETAILS:

PATENT NO PATENT NO KIND WO 9711690 AU 9671686 A Based on

PRIORITY APPLN. INFO: US 1996-672215

19960625; US 1995-4626P

19950929

9711690 A UPAB: 19970516 AΒ

Treatment or prophylaxis of a bacterial infection in a mammal, by admin. of a cpd. comprising an inhibitor of a global regulator (IGR) of pathogenesis genes (PG) , is new. Also claimed is a method of treating a bacterial infection by administering an inhibitor of one or more pathogenesis factors modulated by agr, sar, sae or xpr. Also new is a method of screening for an IGR of PG, by determining whether a test cpd. alters the level of activity of that IGR. Also claimed is a method for making an antibacterial agent (ABA), comprising screening for the ABA by measuring the ability of ABA to alter the level of activity of global regulator of PG; and synthesising ABA in sufficient amount for admin. to the patient. Also claimed are pharmaceutical compsns. containing an inhibitor of a global pathogene regulator and a carrier.

USE - The cpds., termed antipathogenics, are of use in both human and veterinary infections. They inhibit the naturally occurring,

Mitra 10/032,950

growth-dependent induction of the P3-driven RNAIII and those downstream virulence factors under its influence. Treatment with the cpds. may have any of the following effects: attenuating host inflammatory response, decreasing load of bacterial toxins, disfavouring colonisation of the host, or aiding clearance of infection by the host, and potentiation of the effect of traditional drugs, either by weakening the bacteria or relocating them to a drug or host factor accessible category.

ADVANTAGE - The method represents a new approach to bacterial infections, in contrast to prior art bactericidal, bacteriostatic, or antibiotic cpds., which either kill the microbes or inhibit their growth. The new method targets bacterial pathogenesis, or virulence factors, reducing or eliminating expression of exoproteins, toxins, or other pathogenic factors, associated with specific genes. Even resistant strains of bacteria, partic. staphylococci, most notably S. aureus, which have developed resistance to methicillin or are multi-drug resistant, can be regulated by the cpds. to alter the course of an infection.

Dwg.0/20

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ALIGNMENTS

RESULT 1 AAY67859 Staphylococcus aureus infection; treatment; AgrD; agr response; virulence factor. Staphylococcus aureus AgrDII derived peptide sequence WPI; 2000-147202/13 Muir TW, Mayville P, (UYRQ) UNIV ROCKEFELLER.
(UYNY) UNIV NEW YORK STATE. 24-JUN-1998; 24-JUN-1999; 29-DEC-1999. WO9967286-A2 Staphylococcus aureus. 25-APR-2000 AAY67859; AAY67859 standard; peptide; 9 (first entry) 98US-0103438 99WO-US14562 Novick RP, A Ĵ. ģ Beavis

New cyclic peptides for treating infections with Staphylococcus aureus

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                                                            This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
                                                                                                                                                                                                                                            New cyclic peptides for treating infections with Staphylococcus aureus
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The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AM50899-906). The peptide corresponds to the Staphylococcus aureus AgrDII sequence with a Cys5 to Ser mutation (lactone). It was synthesised on a Wang-resin using an Fmoc N-alpha protection strategy. Following chain assembly the peptide was cleaved from the support and the Ser-5 residue deprotected by treatment with a trifluoroacetic acidianisole:water mixture (90:5:5) for 4 hr. The partially protected peptide-alpha carboxylates were then dissolved in DMF and treated with PyBOP and a catalytic amount of dimethylaminopyridine. Cyclization was complete after 2 hr. The remaining protecting groups were then The cyclic peptide is capable of inhibiting the agr response of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgrD2; agr infection;
The present sequence is that of a novel synthetic AgrD2 linear thioester peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrP3 promoter. This allowed activation or inhibition of the agr present to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone cyclic peptide (see AAMS1001), the present peptide was unable to either activate or inhibit the agr response, even
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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UNIV NEW YORK STATE.
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8; Conser
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                                                                                                                                                                                                                               cyclic AgrD-autoinducing peptide for bacterial for treating Staphylococcus aureus infection in a
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                             free acid peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrD3 promoter. This allowed activation or inhibition of the agrD3 promoter. This allowed activation or inhibition of the agrD3 promoter cyclic peptide (see AMM51001), the present peptide was unable to either activate or inhibit the agr response, even was unable to either activate or inhibit the agr response, even considered cyclic peptides (see AMM5009) on and methods for preparing them. The cyclic peptides are useful for infection
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                                                                                                                                                                                                                                                             Example 1; Column 9; 18pp; English
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Pred. No. 9.3e+05;
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The present sequence is that of a novel synthetic AgrD2 lactone cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactone bond. The peptide is derived from an AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrD3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. The lactone AgrD2 peptide inhibited the agr response of group I S. aureus strains without activating the agr response in group I, II or III strains. The invention provides claimed cyclic peptides (see AM50899-906 and AAM5099) and methods for preparing them, especially peptides where the cyclic bond is a lactam or lactone bond. The cyclic peptides are useful for bacterial interference, cespecially for the treatment of S. aureus infection.
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Best Loc Matches Query Match

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Score 38; Pred. No.

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Matches 8
                                  The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Synegistic antiblotic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated
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                                                                                                                                                                                                                                                Use of autoinducer-2 agonists or antagonists for regulating activity autoinducer-2 receptor, regulating bacterial growth and pathogenesis
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(QUOR-)
(UYTE-)
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 Sequence
                         quorum sensing.
                                                                                                                                                                                                             Disclosure; Page 33; 134pp; English
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07-DEC-2000; 2000US-254398P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide-mediated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB07160 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                          2002-075235/10
                                                                                                                                                                                                                                      antibiotic compositions
                                                                                                                                                                                                                                                                                                                                           UNIV PRINCETON.
QUOREX PHARM INC.
UNIV TECHNOLOGIES
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  9 AA;
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                                                                                                                                                                                                                                                                                                                   Dammel CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quorum sensing inhibitor peptide cyclo-XII
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                                                                                                                                                                                                                                                                                                                   Schauder S,
                                                                                                                                                                                                                                                                                                                                             TNT
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                                                                                                                                                                                                                                                                                                                                             INC
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                                                                                                                                                                                                                                                                                                                   Shokat K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dermatological;
e regulator; cyclic.
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RESULT 9
AAY67861
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                                                                                                                                                                                         Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                          This sequence represents a cyclic peptide derived from the Staphylococcus aureus AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
                                                                                                                                                                                                                                                                                                                                                                                                              New cyclic peptides for
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-147202/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muir TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus infection; cyclic peptide; AgrD; virulencs factor; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. aureus peptide #1 used for bacterial interference.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY67851 standard; peptide; 9 AA
Staphylococcus aureus infection; AgrD; agr response; treatment;
                    Staphylococcus aureus AgrDII derived peptide sequence
                                                                                        AAY67861 standard; peptide; 9 AA
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 26; 37pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-1998;
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                                            25-APR-2000
                                                                    AAY67861;
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                                                                                                                                                                                         l Similarity
9; Conserv
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                                                                                                                                                GVNAXSSLF 9
                                                                                                                                                                     GVNAXSSLF 9
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                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                         AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEW YORK STATE.
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                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
/label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                       94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novick
                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                              treating
                                                                                                                                                                                             0
                                                                                                                                                                                                       Score 37;
Pred. No.
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                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               infections with Staphylococcus aureus
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                                                                                                                                                                                                       DB 21; I
. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beavis
                                                                                                                                                                                                                  Length
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                                                                                                                                                                                             Indels
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                                                                                                                                                                                            Gaps
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RESULT 10
ABP53540
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                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                    peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibite the agr response, which is normally associated with the release of virulence factors of staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virulence factor.
                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the Staphylococcus aureus AgrDII derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cyclic peptides for treating infections with Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-147202/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muir TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus
27-DEC-2001; 2001US-0032950
                                                                                                       Synthetic
                                                                                                                          Cyclic peptide; Staphylococcus aureus; infection; antibacterial; agr response inhibitor.
                                                                                                                                                          Cyclic peptide
                                                                                                                                                                                13-DEC-2002
                                                                                                                                                                                                      ABP53540
                                                                                                                                                                                                                         ABP53540 standard; peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Examples; Page 22; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNQ ) UNIV ROCKEFELLER (UYNY ) UNIV NEW YORK ST
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                    20-JUN-2002.
                                                                         Misc-difference
                                         US2002077453-A1
                                                                                                                                                                                                                                                                                                                        Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                GVNAXSSLF
                                                                                                                                                                                                                                                                               GVNAXSSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mayville P,
                                                                                                                                                                                                                                                                                                                                                                   9 AA;
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                 (first entry)
                                                                                                                                                           SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0103438
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/label= Unknown
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                                                                                  Location/Qualifiers
                                                             /note= "any amino acid"
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                                                                                                                                                                                                                                                                                                                                  94.9%;
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                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                  Score 37;
Pred. No.
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                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                        DB 21; I
9.3e+05;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beavis R;
                                                                                                                                                                                                                                                                                                                                            Length 9;
                                                                                                                                                                                                                                                                                                                           Indels
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RESULT 11
AAM50899
ID AAM50
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Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                        ABP53540 to ABP53547 represent cyclic peptides (I) from the present invention. The present invention also describes a method for treating Staphylococcus aureus infection comprising the administration of a composition comprising (I). (I) has antibacterial activity, and can used as an agr gene response inhibitor. The peptides are useful for treating S. aureus infections.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cyclic peptides, useful infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MUIR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1998;
24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 10; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-681366/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muir TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVI/)
                                                                                                                                                                                                                                                                                          AAM50899 standard; Peptide;
                                                                                                                                                                                                            Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
                                                                                                                                                                                                                                     AgrD-autoinducing cyclic peptide, inhibitor of
                                                                                                                                                                                                                                                        08-MAY-2002
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                                                                                                                       Misc-difference
                                                                                                                                                 Misc-difference
                                                                                                                                                                                           Synthetic
                                                                     08-JAN-2002
                                                                                     US6337385-B1
                                                                                                                                                                   Misc-difference
                                  24-JUN-1998;
                                                   24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                       Local Similarity hes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUIR T W.
) MAYVILLE P.
) NOVICK R P.
) BEAVIS R.
) JI G.
                                                                                                                                                                                                                                                                                                                                                       1 GVNAXSSLF 9
          UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mayville P,
                                                                                                                                                                                                                                                                                                                                      GVNAXSSLF
                                                                                                                                                                                                                                                                                                                                                                                                          9 AA;
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-090402P
99US-0339511
                                                                                                                                 /note=
                                   98US-090402P
                                                    99US-0339511
                                                                                                                                                                   Location/Qualifiers
                                                                                                                /note=
                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                     94.9%; but
100.0%; Pr
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                                                                                                                                "note linked to peptide"
                                                                                                                                                          "any amino acid"
                                                                                                                "note linked to
                                                                                                       peptide"
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                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB; Pred. No. 9.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beavis
                                                                                                                                                                                                                                                                                                                                                                      DB 23;
5. 9.3e+05;
0;
                                                                                                                  residue 5
                                                                                                                                           residue 9 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus
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                                                                                                                                                                                                                                        agr response
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                                                                                                                                          cyclic
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RASSULT 12
AAM50908
ID AAM50
XX AAM50
XX O8-MA
DT O8-MA
XX Staph
KW Staph
KW antil
XX Synth
XX Key
FH Modii
FT Misc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biosynthetic amino acid, n is 0-10 and y is 1-10. The cyclic bond is especially a lactam or lactone bond. The thiololactone is especially a lactam or lactone bond. The thiololactone structure within native AgrD peptides is required for activation of the agr response. Elimination of the thiol ester component of the cyclic ring structure can destroy agr response activating activity while preserving and enhancing inhibitory activaty. A claimed method of preparing a cyclic peptide involves: assembling a linear peptide chain on to a solid phase resin support; deprotected peptide with neutral buffer for a time sufficient to constitute the cyclic peptide and cleave the peptide from the support; and recovering the cyclic peptide. The peptide is useful for bacterial interference, especially for the treatment of S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is a secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 controls the Synthesis or referred proteins responsible for pathogenicity in S. aureus. Preferred proteins may have the sequence NH2-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z residue and COOH other than a thioester bond, where X is an amino acid, an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a synthetic or a peptidomimetic amino acid, n is 0-10 and y is 1-10. The cyclic bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muir TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                               Staphylococcus antibacterial;
                                                                                                                                                                                                                                                                                                 Protected
                                                                                                                                                                                                                                                                                                                                  08-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                               AAM50908 standard; Peptide; 9
                                 Misc-difference
                                                                                                                                 Modified-site
                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection.
                                                                Modified-site
                                                                                                  Modified-site
                                                                                                                                                                  Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVNAXSSLF
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                                                                                                                                                                                                                                                                                             peptide used in cyclic peptide production.
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                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                               aureus; AgrD; agr response; infection; therapy; cyclic.
                                                                                                                                                                               Location/Qualifiers
                                                 /note=
                                                                                  /note=
                                                                                                                                                 note= "Z-Gly"
                                                                                                                   'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.9%;
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 "note linked to residue 9 to form cyclic peptide"
                                                    "Ser(Bzl)"
                                                                                    "Ser(Bzl)"
                                                                                                                   Dpr (Boc)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23; I
. 9.3e+05;
ches 0;
                                                                                                                                                                                                                                                                    inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Į.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                        antibiotic;
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/note=

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RESULT 13
ADM51005
ID ADM51
XX ADM51
AC ADM51
XX 08-M2
XX 08-M2
XX 08-M2
XX infec
XX AgrD2
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AMM50899-906). The peptide corresponds to the staphylococcus acreus AgrDII sequence with a Cys5 to diaminopropionic acid (Opr) mutation (lactam). It was synthesised on a Wang-resin using an Fmoc N-alpha protection strategy. Following chain assembly, the peptide was cleaved from the support and the Dpr-5 residue deprotected by treatment with a trifluoroacetic acid:anisole:water mixture (90:55) for 4 hr. The partially protected peptides alpha carboxylates were then dissolved in DMF and treated with PyBOP. Cyclization was complete after 2 hr. The remaining protecting groups were removed by treatment with HF and the peptide purified by HFLC. The cyclic peptide is capable of inhibiting the agr response of Staphylococcus aureus. The thioloactone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure with a lactam (as in the present case) or a lactone can destroy agr response activating activity while preserving and chancing inhibitory activity. The cyclic peptides are useful for infection
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Best Local S
Matches
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     Stpahylococcus Synthetic.
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                                                                           AgrD2; agr infection;
                                                                                                                                                       AgrD2 lactam
                                                                                                                                                                                                           08-MAY-2002
                                                                                                                                                                                                                                                            AAM51005;
                                                                                                                                                                                                                                                                                                          AAM51005 standard; Peptide; 9 AA
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UNIV NEW YORK STATE
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                                                                           therapy; cyclic.
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                                                                                                    response; inhibitor; antibiotic; antibacterial;
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                                                                                                                                                     cyclic
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; F1
                                                                                                                                                     peptide
                                                                                                                                                                                                        entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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RESULT 14
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                                                                                                                                                                                                                                                                                             The present sequence is that of a novel synthetic AgrD2 lactam CC cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactam bond. The peptide 1s derived from an AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological cativity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrp3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. The AgrD3 lactam peptide inhibited the agr response in group I S. aureus strains and did not activate the agr response in group I S. aureus strains. The invention provides claimed cyclic peptides (see CAMS0899-906 and AAMS0999) and methods for preparing them, captic peptides are useful for bacterial interference, cespecially for the treatment of S. aureus infection.
                                                                                                                                                                                                                    Query Match
Best Local S
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-170774/22.
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                                                   13-MAR-2002
                                                                                                                                                                                                                                                                        Sequence
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                       Peptide-mediated quorum sensing inhibitor peptide cyclo-XIII.
                                                                           ABB07161;
                                                                                                      ABB07161 standard; peptide; 9 AA
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9; Conserv
                                                                                                                                                                     1 GVNAXSSLF 9
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                                                                                                                                                                                      GVNAXSSLF
                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                    conservative
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    peptide"
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                                                   entry.
                                                                                                                                                                                                                                   94.9%; Score 37;
100.0%; Pred. No.
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9.3e+05;
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Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological:

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AAW38323
ID AAW38
XX AAW38
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Synergistic antiblotic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated quorum sensing.
                                                                                             Transcription inhibitory peptide; inhibition; antibiotic; abscesses; endocarditis; pneumonia; osteomyelitis; virulence factor; agr regulator; agr-rnaIII gene; colonisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 33; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of autoinducer-2 agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis, also antibiotic compositions \,\cdot\,
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(QUOR-)
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07-DEC-2000;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                          Staphylococcus aureus.
                                                                                                                                                                                                   Transcription
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                                                                                                                                                                                                                                                                                                                                              AAW38323 standard;
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QUOREX PHARM INC.
UNIV TECHNOLOGIES
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Similarity 100.0%;
9; Conservative (
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2000US-254398P.
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                                                                                                                                                                                                 inhibitory peptide 3.
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                                                                                                                                                                                                                                                                                                                                              peptide;
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Pred. No.
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. 9.3e+05;
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CC This novel peptide sequence (or it's analogue) inhibits agr-rnalII cranscription in Staphylococcus aureus (S. aureus), and is 9 amino acids CC long. The peptide can be added to pharmaceutical compositions to treat CC or prevent infections or diseases caused by S. aureus in animals, and CC especially in humans. They can also be combined with traditional CC antibiotics. S. aureus causes conditions ranging from abscesses (boils CC antibiotics) to life-threatening infections e.g. endocarditis, prevents, osteomyelitis, by secreting injurious proteins, or virulence CC factors. The synthesis of virulence factors is controlled by the agr regulator, which activates transcription of the agr-rnalII gene to produce RNAIII, which induces transcription of the genes encoding the CC virulence factors. The peptides inhibit agr-rnaIII transcription in and therefor virulence factor expression. The peptides can also be used in vitro to prevent Staphlococcus aureus colonisation.
                                                                                                                                                                                                                                                                                                                                            Peptide inhibiting agr-rnalII transcription in \mbox{-} useful to treat S. aureus infection
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                                                                                                                                                                                                                                                                                                           Claim 7; Page 15; 24pp; English
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/note= "linked to the carboxy terminus via a cyclic thicester bond"
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Search completed: January 29, Job time: 35.0735 secs 2004, 14:52:10

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Matches Query Match Best Local

Similarity 8; Conserv GVNAXSSLF GVNACSSLF

Conservative

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Score 36; Pred. No. Mismatches

DB 19; 9.3e+05;

Length 9;

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Gaps

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1: pir1:*
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GVNAXSSLF 9
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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T27215
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	ALIGNMENTS					
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beta-glucosidase-	T47837		514			42
hypothetical prot	C96744		480	•		41
Similar to Cytochr	D86306		476			40
hypothetical prote	T24523		468			39
manganese transpor	AF2539		442	•		38
maltose/maltodextr	C83902	N	424	71.8	28	37
maltose/maltodext	C70038		421			36
ubiquinol-cytochr	S12023		381	•		35
ubiquinoi-cytochr	A53224		381			34
hypothetical prot	E64499		350	•		ω G
iron(III) dicitrat	S74439		349			32
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hypothetical prote	F90350		271	•		30

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-47 <KUR> A;Cross-references: GB:BA000018; PID:g13701831; PIDN:BAB43124.1; GSPDB:GN00149 A;Experimental source: strain N315 C;Genetics: AgrD protein [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: C89995 R;Kurdda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, T.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1255-1240, 2001 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: C89995 RESULT 2 A28067 망 Ş A;Gene: agrD C89995 Best Loc Matches Query Match Local 24 GUNACSSLF 32 Similarity 8; Conserv GVNAXSSLF 9 Conservative 92.3%; Score 36; DB 2 88.9%; Pred. No. 0.11; tive 0; Mismatches DB 2; Length 47; Indels 0 Gaps 0

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lysosomal membrane glycoprotein LAMP-1 - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 20-Aug-1999 C;Accession: A28067 R;Chen, J.W.; Cha, Y.; Yuksel, K.U.; Gracy, R.W.; August, J.T. J. Biol. Chem. 263, 8754-8758, 1988 A;Biol. Chem. 263, 8754-8758, 1988 A;Title: Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycopr A;Reference number: A28067; MUID:88243732; PMID:3379044 A;Accession: A28067; MUID:88243732; PMID:3379044

A;Molecule type: mRNA A;Residues: 1-382 <CHE> A;Cross-references: GB:J03881; NID:g198706; PIDN:AAA39411.1; PID:g293692 A;Note: the authors translated the codon ATT for residue 1 as Leu and CCG C;Superfamily: lysosome-associated membrane protein C;Keywords: glycoprotein; membrane protein

for

residue

Query Match Best Local Matches

Local Similarity 77.1 hes 7; Conservative

89.7%; Score 35; D 77.8%; Pred. No. 2;

DB 2;

1; Mismatches

Length 382; 1; Indels

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C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 03-May-1996
C;Accession: A60534
                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 22-407 <mr/>
A;Residues: 22-407 <mr/>
A;Residues: 22-407 <mr/>
A;Cross-references: EMBL:X14765; NID:g56577; PIDN:CAA32873.1; PID:g56578
A;Note: part of this sequence, including the amino end of the mature protein,
C;Superfamily: lysosome-associated membrane protein
C;Keywords: glycoprotein; membrane protein
C;Keywords: glycoprotein; membrane glycoprotein, 107K #status experimental •
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R;Heffernan, M.; Yousefi, S.; De
Cancer Res. 49, 6077-6084, 1989
A;Title: Molecular characterizat
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 C;Species:
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A;Reference number: S03331; MUID:89153580; PMID:2920835
A;Accession: S03331
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:J03672
A;Note: the authors translated the codon GGG for residue 15 as R;Himeno, M.; Noguchi, Y.; Sasaki, H.; Tanaka, Y.; Furuno, K.; FEBS Lett. 244, 351-356, 1989
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A; Residues: 1-407 < HOW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Rattus norvegicus (Norway rat);Date: 18-Oct-1989 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999;Accession: A30200; S03331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Title: Molecular characterization of P2B/LAMP-1, a major;Reference number: A60534; MUID:90002989; PMID:2676155
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: C69812
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Ber C; Bxcn, S; Broullet, S; Bruschi, C.V.; Caldwell, B; Capuano, V; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Ehtian, K.D.; Errington, J; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M Koetter, P.; Koningstein, G.; Krogh, S; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau V, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadoie, Y.; Sato, T.; Scanl A;Authors: Schleich, S.; Schroeer, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsytta, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Seference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor-protein kinase-like protein - Arabidopsis thaliana
N;Alternate names: protein f26013.190
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000
kpsD protein - Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 16-Jul-1999
C;Accession: S36653; E48492; C42644
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S36653
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A; Note: F26013.190
C; Superfamily: una
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A;Residues: 1-895 <DEL>
A;Cross-references: EMBL:AL133452
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A; Accession: T45786
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C; Superfamily:
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source: strain
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                                                                                                                                                                                                                                                                                                               82.1%;
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77.8%;
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168
                                                                                                                                                                                                                                                                                                               Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                        2.
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1; Mismatches
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abase, December 1999
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2.9;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 22-389 <PAZ>
A;Residues: 22-389 <PAZ>
A;Cross references: GB:X74567
A;Cross references: GB:X74567
CB:Steenbergen, S.M.; Wrona, T.J.; Vimr, E.R.
J. Bacteriol. 174, 1099-1108, 1992
A;Title: Functional analysis of the sialyltransferase complexes in Escherichia coli
A;Reference number: A42644; MUID:92138601; PMID:1735705
A;Accession: C42644
A;Accession: C42644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Pazzani, C.; Rosenow, C.; Boulnois, G.J.; Bronner, D.; Jann, K.; Roberts, I.S. J. Bacteriol. 175, 5978-5983, 1993
A;Title: Molecular analysis of region 1 of the Escherichia coli K5 antigen gene cluster: A;Reference number: A48492; MUID:93388530; PMID:8397187
A;Accession: E48492
  RESULT 9
D69750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: E81286
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A;Residues: 106-125, 'D', 127-244,'N',246-297,'S',299-300,'VI',303-379,'M',381-385,'W',387
A;Cross-references: GB:M76370; NID:g146947; PIDN:AAA24214.1; PID:g146950
A;Experimental source: K1, strain EVI
A;Experimental source: K1, strain EVI
A;Note: sequence extracted from NCBI backbone (NCBIN:79370, NCBIP:79381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, A;Reference number: $36649 A;Accession: $36653
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: E81286
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C;Superfamily: kpsD protein
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C;Species: Campylobacter jejuni
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A;Molecule type: DNA
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Experimental source: serotype (
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Best Local
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                                                                                                                                                                                                                                                                                              Genetics:
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Similarity 87.5%;
7; Conservation
                                                                                                                                                                 Similarity 7; Conserv
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                                                                                  GVNANSSL 133
                                                                                                                                                                                                                                               kpsD protein
                                                                                                                                                                     Conservative
                                                                                                                                                                                     79.5%;
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O2, strain NCTC 11168
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Pred. No. 18;
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Pred. No. 19;
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    Campylobacter jejuni

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RESULT 11
A99227
hypothetical
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C;Accession: D69750
C;Accession: D69750
C;Accession: D69750
C;Accession: D69750
C;Accession: D69750
C;Accession: D69750
C;Brown, S; Broundllet, S; Bruschi, C.V.; Caldwell, B; Capuano, V.; Carter, N.M.; C.; Brown, S; Brown, S; Bruschi, C.V.; Caldwell, B; Capuano, V.; Carter, N.M.; C.; Enrington, J.; Fabret, C.; Ferrari, A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, A; Luture 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, A; Authors: Lauber, U.; Lea, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauuy, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanla, Authors: Schleich, S.; Schroeter, R.; Scoffene, F.; Sekiguchi, J.; Sekowska, A.; Seakeuchi, M.; Tamakschi, A.; Tanaka, T.; Terpsetra, P.; Tognon, A.; Tosato, V.; Uchiyan T.; Hitle: The complete genome sequence, F.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Accession: D69750
                                                                                                                                                                                                                                             A;Gene: SGD:SEC24; SEC24; MIPS:YIL109c
A;Cross-references: MIPS:YIL109c; SGD:S0001371
A;Map position: 9L
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: $48463
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-J
C;Date: 05-Dec-1997
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                                                                                                                                                                                                                     A; Description: involved in endoplamic reticulum to
                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-926 < BOW >
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: protein YIL109c C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEC24 protein - yeast (Saccharomyces cerevisiae)
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A; Residues: 1-631 < K
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                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
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                                                                                                 Best Local
Matches
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Best Local
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787
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6; Conser
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INATSSLF
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                                                                                                          Pred. No. 48;
1; Mismatches
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Pred. No.
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Pred. No.
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                                                                                                                                                             Length 926;
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protein SS00775 [imported] -

Sulfolobus solfataricus

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A;Cross-references: GB:AE006641;
C;Genetics:
A;Gene: SS00775
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A;Molecule type: DNA
A;Residues: 1-109 <KUR>
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A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: A99227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable sugar-binding protein YP00856 [imported] - Yersinia pestis (strain C;Species: Yersinia pestis C;Dace: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001 C;Accession: AD0105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A99139
A;Accession: A99227
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A; Residues: 1-420 < KUR>
A; Cross-references: GB:
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A;Cross-references: EMBL:AC004521; NID:g3128166; PIDN:AAC16095.1; PID:g3128191
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fuj
                                                            A;Status: translated from A;Molecule type: DNA A;Residues: 1-560 <ROU>
                                                                                                                                                                  C;Accession: T02404; B84879
R;Rounaley, S.D.; Lin, X.; Ketchum, submitted to the EMBL Data Library, A;Description: Arabidopsis thaliana
                                                                                                                                                                                                                            probable beta-glucosidase homolog F4II.30 - Arabidopsis thaliana ("Species: Arabidopsis thaliana (mouse-ear cress) ("Species: Arabidopsis thaliana (mouse-ear cress) ("Species: Arabidopsis thaliana (mouse-ear cress) ("Species: Nar-1999 #sequence revision 05-Mar-1999 #text_change 16-Feb-2001 ("Accession: T02404, B84879")
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                                                                                                                         A; Reference number: Z14667
A; Accession: T02404
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Pred.
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                                                                                                                                                                    K.A.; Crosby, M.L.; Brandon, R.C.; Syken
May 1998
chromosome II BAC F4II genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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      Town, C.D.; Fujii,
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submitted to the EMBL Data Library, September 1997 A;Reference number: Z20330
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T27215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 2
A;Introns: 3/2; 33/3; 76/3; 102/1; 157/2; 242/3;
C;Superfamily: Agrobacterium beta-glucosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE002093; NID:g3128191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-560 <STO>
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euss, D.; Nierman, W.C.; W
Nature 402, 761-768, 1999
                                                                                                                                                                                            transcription factor AKR - chicken

NALternate names: avian knotted-related protein; homeotic protein
C;Species: Gallus gallus (chicken)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-
C;Accession: S58439; S58440
R;Ryan, A.K.; Tejada, M.L.; May, D.L.; Dubaova, M.; Deeley, R.G.
R;Ryan, A.K.; Tejada, M.L.; May, D.L.; Dubaova, M.; Deeley, R.G.
submitted to the EMBL Data Library, April 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 4
A; Introns: 70/1; 329/3
C; Superfamily: multidr
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A; Residues: 1-633 <WIL>
A; Cross-references: EMB
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A;Cross-references: EMBL:U25353; NID:g857681; PIDN:AAA83567.1; PID:g857682 R;Ryan, A.K.; Tejada, M.L.; May, D.L.; Dubaova, M.; DeeLey, R.G. Nucleic Acids Res. 23, 3252-3259, 1995
A;Title: Isolation and characterization of the chicken homeodomain protein
                                                                                                                                A;Description: Isolation and characterization A;Reference number: S58439 A;Accession: S58439
                                                                                     A; Molecule type: mRNA
A; Residues: 1-269 < RYA>
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ce: clone Y57G11C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resistance protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSPDB:GN00139
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A;Reference number: $58440; MUID:95396587; PMID:7667102
A;Accession: $58440
A;Accession: $18440
A;Accessio
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 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen, Ltd
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Result No.

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s SWISS-PROT entry is copyright. It is produced throug ween the Swiss Institute of Bioinformatics and the Buropean Bloinformatics Institute. There are no res by non-profit institutions as long as its content ifsed and this statement is not removed. Usage by a lites requires a license agreement (See http://www.isbities requires a license agreement	- PRING OF AND N-GLYCOSYLATED; SOME OF THE N-GLYCANS ATTACHED TO LAMP-1 ARE POLYLACTOSAMINOGLYCANS (BY SIMILARITY) PRINTIARITY: BELONGS TO THE LAMP FAMILY.	-1- FUNCTION: PRESENTS CARBOHYDRATE LIGANDS TO SELECTINS. ALSO IMPLICATED IN TUMOR CELL METASTASIS1- SUBCELLULAR LOCATION: Type I membrane protein. Lysosomal111S PROTEIN SHUTTLES BETWEEN LYSOSOMES, ENDOSOMES, AND THE PLASMA	DISULEIDE BONDS, MEDLINE=90237040; FubMed=2332434; Arterburn L.M., Earles B.J., August J.T.; "The disulfide structure of mouse lysosome-associated membrane protein 1."; J. Taiol. Chem. 265.7419.7423(1990)	NA cione encoding ce similarity to	F 25-406 FROM N.A., AND PARTIAL SEQUENCE. 243732; PubMed=3379044; Cha Y., Yuksel K.U., Gracy R.W., August J.T.;	SEQUENCE FROM N.A. Heffernan M., Yousefi S., Dennis J.W.; Submitted (FEB-1990) to the EMBL/GenBank/DDBJ databases.	s A.; serization and cloning of lgp110, a lysosomal memberization mouse and rat cells."; Chem. 265:12036-12043(1990).	<pre>[1] SEQUENCE FROM N.A. MEDLINE=90307738; PubMed=2142158; Grander B.L., Green S.A., Gabel C.A., Howe C.L., Mellman I.,</pre>	LAWRI CK LAWR'L. MUS MUSCULUS (MOUSE). MUS MUSCULUS (MOUSE). EUKARYOTA; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;	01-OCT-1989 (Rel. 12, Created) 01-OCT-1989 (Rel. 15, Last sequence update) 01-NUG-1990 (Rel. 15, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (LGP-A) (LGP-120) (CD107A) (P2B).	1 IP1 MOUSE

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01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1)
kDa lysosomal membrane glycoprotein) (LGP-120) (CD107A).

LAMP1 OR LAMP-1.
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PROSITE; PS00311; LAMP 2; 1.
Transmembrane; Glycoprotein; Lysosome; Signal.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBI_TaxID=10116;
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Pfam; PF01299; Lamp; 1.
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EMBL; M34959; AAA41525.1; -.
EMBL; X14765; CAA33873.1; -.
EMBL; U75406; AAA19108.1; -.
PIR; A30200; A30200.
InterPro; IPR002000; Lamp.
Pfam; PF01299; Lamp; 1.
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STRAILWWistar Kyoto; TISSUE-Apartic smooth muscle;
Adams L.A., Werny I., Schwaftz S.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PRESENTS CARBOHYDRATE LICANDS TO SELECTINS.
-!- SUBCELLULAR LOCATION: Type I membrane protein. Lysoson
-!- SUBCELLULAR LOCATION: Type I membrane protein. Lysoson
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SEQUENCE FROM N.A.
MEDLINE=89017240; PubMed=3174652;
Howe C.L., Granger B.L., Hull M.,
Mellman I.;
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Sakaki Y., Kato K.;
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AC P42218;

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DT 01-NOV-1995 (Rel. 32, Las
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OS Escherichia coli.

OC Enterobacteria; Proteobacteria;

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OX NCBI_TAXID=562;

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RP SEQUENCE FROM N.A.

RC STRAIN=5338530; PubMed-
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PIR; S36653; S36653.
Pfam; PF05159; Capsule_synth; 1.
Polysaccharide transport; Transport.
SEQUENCE 389 AA; 46381 MW; 73058122C28027DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular analysis of region 1 of the Escherichia coli K5 antigen gene cluster: a region encoding proteins involved in cell surface expression of capsular polysaccharide.";

J. Bacteriol. 175:5978-5983(1993).
LMP1_CRIGR P49129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Rosenow C., Boulnois G.J.,
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    PRINTS; PRO0336; LYSASSOCTDMP.
PROSITE; PS00310; LAMP_2; 1.
PROSITE; PS00311; LAMP_2; 1.
Transmembrane; Glycoprotein; Lys
SIGNAL 1 21 BY
CHAIN 22 407 LYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Rodentia; Sciuros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
101-OCT-1996 (Rel. 34, Last annotation update)
Lysosome-associated membrane glycoprotein 1 p
(Lysosomal membrane glycoprotein A) (LGF A).
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NCBI_TaxID=10029;
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MEDLINE=97021428; PubMed=8867788;
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"Cell surface accumulation of overexpressed
   Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Cricetinae;
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ebrlich S.D., Emmerson P.T.,
RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Mediue C.,
RA Medina N., Mellado R.P., Mizuno N., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Raivolta C., Rocha E., Roche B., Rose M., Sadale V.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Socffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Socffone F.,
RA Takeuchi M., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tacconi E., Takagi T., Tarahashi H., Takemaru K.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vasarotti A.,
"The Complete genome sequence of the Gram-positive bacterium Bacillus
RT Subtilis.";

"The Complete genome sequence of the Gram-positive bacterium Bacillus
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15-JUL-1998
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P39816;
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Submitted (JUL-1997) to the E
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Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98044033; PubMed=9384377;
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SEQUENCE OF 515-631 FROM N.A. STRAIN-168 / 6GM; BTRAILNE-95270606; PubMed=7751298; Tolner B., Ubbink-Kok T., Poolman
                                                                                      "The complete subtilis.";
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system IIABC component ybfS (EC
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 B., Konings W.N.;
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EMBL; Z99105; CAB12029.1; -.
EMBL; U5147; AAA82877.1; -.
EMBL; U5147; AAA82877.1; -.
PIR; D69750; D69750.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
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                                                                                        Similarity 75.
                                GINAASSL 179
                                                            GVNAXSSL
                                                                                                                                                478
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77
106
1149
1173
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2243
2350
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Phosphorylation;
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                                                                                                                                                                 68144 MW;
                                                                                                    79.5%;
75.0%;
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EILE DOMAIN.
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EILE DOMAIN.
FOTENTIAL.
POTENTIAL.
                                                                                        Score 31; DB Pred. No. 17; 1; Mismatches
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Length 631; Indels

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Gaps

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Subbilist, EG11014; ybfs.
Interpro; IPR001127; PTS_EIIA.
Interpro; IPR0011956; PTS_EIIB.
Interpro; IPR001352; PTS_EIIC.
Pfam; PP00357; PTS_EIIG.; 1.
Pfam; PP00357; PTS_EIIG; 1.
Pfam; PP00367; PTS_EIIG; 1.
Pfam; PP002743; PTS_EIIB; 1.
ProDom; PD0012743; PTS_EIIB; 1.
ProDom; PD0012743; PTS_EIIB; 1.
ProDom; PD001476; PTS_EIIB; 1.
ProDom; PD001476; PTS_EIIB_910; 1.
TIGRPAMS; TIGR00830; PTBA; 1.
PROSITE; PS00371; PTS_EIIA_1; 1.
PROSITE; PS00371; PTS_EIIA_1; 1.
PROSITE; PS00375; PTS_EIIA_1; 1.
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J. Bacteriol. 177:2863-2869(1995).

-i. FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (FTS). A MAJOR CARBOHYDRATE ACTIVE -TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL, THE IIA DOWAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHORYLATION SITE (THE DONO
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CATALYTIC ACTIVITY: Protein N-phosphohistidine + histidine + sugar phosphate.

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: Contains 1 PTS EIIA domain.

SIMILARITY: Contains 1 PTS EIIB domain.

SIMILARITY: Contains 1 PTS EIIB domain.
               PS00371; PTS_EIIA_1; 1.
PS01035; PTS_EIIB_CYS; 1.
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RESULT 6
SC24_YEAST
ID SC24_Y
     GGD; S0001371; SEC24.
GO; GO:0005515; F:protein binding acti
GO; GO:0006514; F:autophagy; IMP.
InterPro; IPR001974; Gelsolin.
InterPro; IPR006906; Sec23_belical.
InterPro; IPR006996; Sec23_trunk.
InterPro; IPR006895; zf-Sec23_Sec24.
Pfam; PF04811; Sec23_trunk; 1.
Pfam; PF04811; Sec23_trunk; 1.
Pfam; PF04810; zf-Sec23_Sec24; 1.
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01-FEB-1995
                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=20177547; PubMed=10712514;

MEDLINE=20177547; PubMed=10712514;

Hamamoto S., Gimeno R.E., Kaiser C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20219212; PubMed=10753972; Peng R., De Antoni A., Gallwitz D.; "Evidence for overlapping and distinct functions in protein transport of coat protein Sec24p family members."; J. Biol. Chem. 275:11521-11528(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=9169870;
Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
Nature 387:84-87(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
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15-SEP-2003
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Yoshihisa T.;
                                                                                                                                                                                                                  PIR; S48463; S48463.
PDB; 1M2V; 20-SEP-02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cerevisiae."
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STRAIN=S288c / AB972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: COMPONENT OF THE COPII COAT, THAT COVERS ER-DERIVED VESICLES INVOLVED IN TRANSPORT FROM THE ENDOPLASMIC REFICULUM TO THE GOLGI APPARATUS. COPII ACTS IN THE CYTOPLASM TO PROMOTE THE TRANSPORT OF SECRETORY, PLASMA MEMBRANE, AND VACUCLAR PROTEINS FROM THE ENDOPLASMIC RETICULUM TO THE GOLGI COMPLEX. SUBCURIT: COMPIE IS COMPOSED OF AT LEAST FIVE PROTEINS: THE SEC23/SICCAPERS AND SARI.

SUBCURLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: BELONGS TO THE SEC23/SEC24 FAMILY. SEC24 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _YEAST
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23_trunk; 1.
Sec23_Sec24; 1.
transport; Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
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                                                                                                                                                                               activity;
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   Endoplasmic reticulum;
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01-NOV-1997
01-NOV-1997
28-FEB-2003
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DOMAIN
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SEQUENCE
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 23:3252-3259(1995).
-!- FUNCTION: BINDS TO THE F' ELEMENT OF THE APOVLDLII GHERPESS ITS TRANSCRIPTION.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE TALE/TGIF HOMEOBOX FAMILY.
-!- SIMILARITY: Contains 1 homeobox domain.
                                                                                              Nuclear protein.
DNA_BIND 35
SEQUENCE 269 A
                                                                                                                                           PRODOM; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; FALSE NEG-
PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                               InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                      EMBL; U25353; AAA83567.1; -. PIR; S58439; S58439.
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95396587; PubMed=7667102;
Ryan A.K., Tejada M.L., May D.L., Dubaova M., I
"Isolation and characterization of the chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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                                                                                                                                  Transcription regulation;
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                                               Similarity 6; Conserv
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GANAQSGLF
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157
926 AA;
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(Rel. 35,
(Rel. 41,
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75.0%;
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Last sequence update)
Last annotation update)
                                                                                               WW.
                                                                                                                                  Repressor; Homeobox; DNA-binding;
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                                               Score 29; DB
Pred. No. 20;
0; Mismatches
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POLY-PRO.
                                                                                              HOMEOBOX (TALE-TYPE)
1074355DCC0C2253 (
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n homeodomain
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InterPro; IPR001899; Gram_pos_ancho:
InterPro; IPR001899; IPXTG.
InterPro; IPR003345; M repeat.
Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF02370; M; 7;
Pfam; PF024650; YSIRK_signal; 1.
PRINTS; PR00015; GPOSANCHOR.
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P16946;
01-AUG-1990
01-AUG-1990
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of a divergent M protein gene and ar "Identification of a divergent M protein gene and ar gene family in Streptococcus pyogenes serotype 49.", J. Bacteriol. 171:6397-6408(1989).
-I- SUBCELLULAR LOCATION: Attached to the cell wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Serotype M49;
MEDLINE=90078078; PubMed=2687231;
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TIGRPAMS; TIGRO1168; YSIRK_signal; 1.
PROSITE; PSSO847; GRAM_POS_ANCHORING; 1.
Virulence; Phagocytosis; Cell wall; Peptidoglycan-anchor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes;
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01-AUG-1990 (Rel. 15, Last seq
28-FEB-2003 (Rel. 41, Last ann
Virulence factor-related M pro
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REPEAT
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| GVNAXSSL 8
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protein precursor.
                                                                  Score 29; DB
Pred. No. 28;
1; Mismatches
                                                                                                                                                  GLY/PRO-RICH (CELL WALL-SPANNING).
LPXTG SORTING SIGNAL (POTENTIAL).
AMIDE-LINKED TO CELL WALL (POTENTIAL);
4AD6D5A72F637839 CRC64;
                                                                                                                                                                                                                                                            C-2.
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2 X REPEATS, TYPE A.
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01-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTLD EC
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PRINTS; PR00084; MTLDHDRGNASE; 1.
PROSITE; PS00974; MANNITOL DHGENASE; 1.
Oxidoreductase; NAD; Complete proteome.

NP BIND
3 14 NAD (BY SIMILARITY)
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STRAIN=06:H1 / CF7
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17).
                                                                                                                                                Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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Ol-OCT-1994 (Rel. 30, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update
Mannitol-1-phosphate 5-dehydrogenase (EC 1.
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-!- SIMILARITY: Belongs to the mannitol dehydrogenase family.
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MEDLINE=22388234; Publ
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     SEQUENCE FROM N.A
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PubMed=12471157;
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75.08;
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Pred. No. 30;
1; Mismatches
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Best Local S
Matches
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EMBL; U00039; AABL8577 1; -.
EWBL; AE000438; AAC76624.1; -.
EWBL; X06794; CAA29954.1; ALT_SEQ.
EMBL; U00345; AAA29561.1; -.
PIR; B65160; B65160.
ECOGEONe; EG010616; mtlD.
                                                                                                       CONFLICT
SEQUENCE
                                                                                                           PROSITE; rooter, recommended by Complete proteome.

Oxidorreductase; NAD; Complete proteome.

NAD (BY SIMILARITY)

NP BIND

A -> R (IN REF. 1 P

COMPLICE

86

86

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novotny M.J., Reizer J., Esch F., Saier M.H. Jr.;
"Purification and properties of D-mannitol-1-phosphate dehydrogenase
and D-glucitol-6-phosphate dehydrogenase from Escherichia coli.";
J. Bacteriol. 159:986-990(1984)
-i- CATALYTIC ACTIVITY: D-mannitol 1-phosphate + NAD(+) = D-fructose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94316500; PubMed=8041620; Sofia H.J., Burland V., Daniels D.L., Plur Analysis of the Escherichia coli genome. region from 76.0 to 81.5 minutes."; Nucleic Acids Res. 22:2576-2586(1994).
                                                                                                                                                          EcoGene; EG10616; mtlD.

HAMAP; MF 00196; -; 1.

InterPro; IPR000669; Mannitol_dh.

Pfam; PF01232; Mannitol_dh; 1.

PRINTS; PR00084; MTLDHDRGNASE.

PROSITE; PS00974; MANNITOL_DHGENF
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Davis T., Yamada M., Elgort M., Saier M.H.
"Nucleotide sequence of the mannitol (mtl)
                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-25.
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STRAIN=K12 / MG1
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Bacteriol. 176:840-847(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             6-phosphate + NADH.
SUBUNIT: Monomer.
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 62
                                                     Similarity 6; Conser
                         GVNAXSSL
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                                                     Conservative
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41139 MW;
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(MtlR) of Esch
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                                                   Score 29; DB
Pred. No. 30;
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RESULT 12
MYTLD SALTI STANDARD; PRT; 382 AA.
AC Q8Z2E0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1
GN MYTLD OR STY4110 OR T3833.
OS Salmonella typhi.
OC Enterobacteriaceae; Salmonella.
OC Enterobacteriaceae; Salmonella.
OX NCB1_TaxID=601;
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RA Churcher C., Mungall K.L., Bentley S.D., Holde
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Matches 6
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30-MAY-2000 (Rel. 39, Last seqn
15-SEP-2003 (Rel. 42, Last anno
Mannitol-1-phosphate 5-dehydron
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Q9XBM6;
30-MAY-2000
30-MAY-2000
15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=1033-5914 / KAY2026;
MEDITIE=21100248; PubMed=11164312;
Otte S. Lengeler J.W.;
"The mtl genes and the mannitol-1-phosphate dehydrogenase
"The stell a pneumoniae KAY2026.";
FEMS Microbiol. Lett. 194:221-227(2001).
-!- CATALYTIC ACTIVITY: D-mannitol 1-phosphate + NAD(+) =
   STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
MEDLINE=21534947; PubMed=11677608;
Parkhill J. Dougan G., James K.D., Thomson N.R.,
Churcher C., Mungall K.L., Bentley S.D., Holden M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
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InterPro; IPR000669; Mannitol_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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PROSITE; PS00974; MANNITOL DHGENASE;
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SIMILARITY: Belongs to the mannitol dehydrogenase family.
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5-dehydrogenase
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l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 29;
Pred. No.
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; D9927E6C068C5344 CRC64;
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Best Local S
Matches 6
                     SEQUENCE FROM N.A.

STRAINLIT2 / SGSC11412 / ATCC 700720;

MEDLINE=21534948; PubMed=11677609;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Lacourtney L., Porwollik S., Ali J., Dante M., Du F., Hou S.

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mul
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan

Ryan E., Sun H., Wilson R.K.;
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STRAIN=TY2 / ATCC 700931;

MEDLINE=22531367; PubMed=12644504;

MEDLINE=22531367; PubMed=12644504;

Deng W., Liou S.-R., Flunkett G. III, Mayhew G.F., Rose D.J.,

Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;

"Comparative genomics of Salmonella enterica serovar Typhi strains
and_CT18.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0084; MTLDHDRGNASE
PROSTIE; PS00974; MANNITOL DHO
OXIGOREDUCTASE; NAD COMPLETE
NP BIND 3 14
SEQUENCE 382 AA; 40869 MW;
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EMBL; AE016847; AA071314.1; -.
HAMAP; MF00196; -; 1.
InterPro; IPR000669; Mannitol dh.
Pfam; PF01232; Mannitol_dh; 1.
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                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                            MTLD OR STM3686
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15-SEP-2003
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Q8ZL67;
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-!- SIMILARITY: Belongs to the mannitol dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 185:2330-2337(2003).
                                                                                                                                                                                                                                                     NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                               Mannitol-1-phosphate 5-dehydrogenase
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42, Last annotation
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Complete proteome.

NAD (BY SIMILARITY)
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serovar Typhimurium
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ou S., Layman D.,
Mulvaney E.,
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InterPro; IPR000669; Mannitol_dh.

InterPro; IPR000669; Mannitol_dh.

Pfam; PF01232; Mannitol_dh; 1.

PRNITS; PR00084; MTLDHDRGNASE.

PROSITE; PR00974; MANNITOL_DHGENASE; 1.

Oxidoreductase; NAD; Complete proteome.

Oxidoreductase; NAD; Complete proteome.

NP_BIND

14

NAD (BY SIMILARITY)

NP_BIND

182 AA; 40899 MW; C5781FBF88C507E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLCYB SYNP7
Q55276;
16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                   the cyanobacterium Synechococcus sp strain PCC7942.";
Plant Cell 6:1107-1121(1994).
-:- FUNCTION: CATALYZES THE DOUBLE CYCLIZATION REACTION WHICH CONVERTS
-:- LYCOPENE TO BETA-CAROTENE AND NEUROSPORENE TO BETA-ZEACAROTENE.
-:- ENZYME REGULATION: INHIBITED BY THE BLEACHING HERBICIDE 2-(4-METHYLPHENOXY)TRIETHYLAMINE HYDROCHLORIDE (MPTA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
              InterPro; IPR000205; NAD_binding.
InterPro; IPR000103; Pyridine_redox.
PRINTS; PR00469; PNDRDTASEII
                                                                                                                                                                                                                                                                                                                          MEDLINE=95003701; PubMed=7919981; Cunningham F.X. Jr., Sun Z., Chamovitz D., F. "Molecular structure and enzymatic function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechococcus sp. (strain Bacteria; Cyanobacteria;
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                                                            EMBL; X74599;

    -!- PATHWAY: Carotenoid biosynthesis.
    -!- SIMILARITY: BELONGS TO THE LYCOPENE CYCLASE FAMILY.

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Similarity 75.0%;
6; Conservative
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                                                                                                                                                                                                                                                                                                             Hirschberg J., Gannt of lycopene cyclase PCC7942.";
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                                                                                                                                                                                                       Carlsson S.R., Fukuda M., Carlsson S.R., Fukuda M., Structure of human lysosomal membrane glycoprotein 1. Assignment "Structure of human lysosomal membrane glycoprotein 1. Assignment disulfide bonds and visualization of its domain arrangement."; J. Biol. Chem. 264:20526-20531(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane glycoprotein 120,000.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sawada R., Jardine K.A., Fukuda M.;
"The genes of major lysosomal membrane glycoproteins, lamp-1 alamp-2. 5'-flanking sequence of lamp-2 gene and comparison of organization in two genes.";
J. Biol. Chem. 268:9014-9022(1993).
POLYLACTOSAMINOGLYCANS.

MEDLINE=91056099; PubMed=2243102;

MEDLINE=91056099; PubMed=2243102;

MEDLINE=91056099; PubMed=2243102;

MEDLINE=9105099; PubMed=2243102;

MEDLINE=910509; PubMed=22431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 28-50; 116-130 AND 163-197. MEDILINE=8906687; PubMed=3198605; Fukuda M., Vittala J., Matteson J., Carlsson S.R.; "Cloning of cDNAs encoding human lysosomal membrane glycoproteins," Cloning of cDNAs encoding human lysosomal membrane glycoproteins, lamp-1 and h-lamp-2. Comparison of their deduced amino acid sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Purification and characterization glycoproteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mane S.M., Marzella L.,
Hildreth J.E.K., August
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90062189; PubMed=2584229;
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"Molecular cloning
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MEDLINE=93312023; rubbecause:
Carlsson S.R., Lycksell P.-O., Fukuda M.;
Carlsson S.R., Lycksell P.-O., Fukuda M.;
"Assignment of O-glycan attachment sites to the hing human lysosomal membrane glycoproteins lamp-1 and land human lysosomal membrane glycoproteins lamp-1 and land human lysosomal membrane IGANDS TO SELB-
-i- FUNCTION: PRESENTS CARBOHYDRATE LIGANDS TO SELB-
IMPLICATED IN TUMOR CELL METASTASIS.

IMPLICATED IN TOPATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wall modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J04182; AAA60382.1;
EMBL; J03263; AAA59524.1;
PIR; A31959; A31959.
GlycoSuiteDB; P11279; -.
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CARBOHYDRATE-LINKAGE SITES IN HINGE REGION,
MEDLINE=93312023, PubMed=8323299;
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PTM: O- A
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SIMILARITY: BELONGS TO THE LAMP FAMILY.
DATABASE: NAME=PROW; NOTE=CD guide CD107a entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd107a.htm".
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CARBOHYD CARBOHYD CARBOHYD Transmembrane; SIGNAL 1 CHAIN 28 CARBOHYD CARBOHYD CARBOHYD CARBOHYD DISULFID DISULFID DISULFID 888 MIM; CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD DISULFID DOMAIN TRANSMEM DOMAIN PRINTS; PR00336; LYSASSOCTDMP.
PROSITE; PS00310; LAMP_1; 2.
PROSITE; PS00311; LAMP_2; 1. InterPro; IPR002000; Lamp. Pfam; PF01299; Lamp; 1. Genew; HGNC:6499; LAMP1 DOMAIN DOMAIN DOMAIN CARBOHYD GO:0005887; C:integral to plasma membrane; GO:0005764; C:lysosome; TAS. GO:0005624; C:membrane fraction; TAS. 129 75 83 102 106 120 28 405 405 282 194 194 227 227 230 337 344 Glycoprotein; 1164 1196 1198 1198 1198 1198 125 1002 O-LINKED
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CYTOPLASMIC (POTENTIAL)
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Search completed: January 29, 2004, 14:53:07 Job time: 6.82353 secs
                                                                                                                       Query Match 74.4%; Score 29; DB 1; Length 416; Best Local Similarity 66.7%; Pred. No. 32; Matches 6; Conservative 1; Mismatches 2; Indels
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ID 03358
AC 0335
AC 0356
AC 
                                                                                                             RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

C SPECISS-S.aureus (strain Mu50), and S.aureus (strain N315);

C SPECISS-S.aureus (strain Mu50), and S.aureus (strain N315);

REDIALME-21311952; PubMed=11418146;

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Yubuzaki J.,

RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Kanehisa M., Ogasawara N., Hayashi H., Hiramateu K.,

"Whole genome sequencing of meticillin-resistant Staphylococcus

Taureus ".

Lancet 357,1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O33586 PRELIMINARY; PRT; 47
O33586;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1999 (TrEMBLrel. 05, Last sequence)
O1-MAR-2002 (TrEMBLrel. 20, Last annotate)
AGRD (AGRD protein)
AGRD (AGRD protein)
AGRD OSAV2037 OR SA1842.1 OR SA8066.
Staphylococcus aureus (strain Mu50 / ATC
Staphylococcus aureus (strain N315), and
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EMBL; AP003364; BAB58199.1;
EMBL; AP003135; BAB43124.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales;
NCBI_TaxID=158878, 158879, 1280;
   Complete
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29 Q9VEI3
5 Q9VEI3
10 Q64087
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10 Q8W750
2 Q9RCW4
10 Q8W750
2 Q9RCW4
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9 Q8W760
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Q9NF913
Q9KH93
Q9KH88
Q9K2U2
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Q9KCM3
Q9KH91
Q9KH91
Q8KQ42
Q8KQ42
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ATCC 700699), and

peptide variants.";

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update)

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Result No.

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RESULT
Q922T9
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Matches 8
             Query Match
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Matches
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Best Local :
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Submitted (APR-2001) to the EMB
EMBL; BC006785; AAH06785.1; -.

InterPro; IPR002000; Lamp;
Pfam; PF01299; Lamp; 1.

PRINTS; PR00336; LYSASSOCTDMP.
PROSITE; PS00310; LAMP_1; 1.

PROSITE; PS00311; LAMP_2; 1.

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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to lysosomal membrane glycoprotein 1 (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                  01-MAR-2002
01-MAR-2002
01-CCT-2002
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                                                                                                           Ono K., Han J.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY069968; AAL58070.1; -.
InterPro; IPR002000; Lamp.
Pfam; PF01299; Lamp; 1.
Pfam; PF01299; Lamp; 1.
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Mammalia; Eutheria;
                                                                       PROSITE; PS00310; LAMP_1; 2.
PROSITE; PS00311; LAMP_2; 1.
SEQUENCE 406 AA; 43879 MW;
                                                                                                                                                                                                                                    Mammalia; Eutheria;
NCBI_TaxID=10090;
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Eukaryota; Metazoa;
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2 (TrEMBLrel. 22,
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; Rodentia;
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           ; Score 35; DB 1; Pred. No. 11; 1; Mismatches
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Last annotation update)
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Pred. No. 0.67
0; Mismatches
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Pred. No. 4.8;
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                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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Best Local S
Matches 7
                                                                                      034933;
01-JAN-1998
01-JAN-1998
01-JUN-2002
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Lysosomal membrane glycoprotein 1.
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PROSITE; PS00311; LAMP 2; 1.
SEQUENCE 407 AA; 43936 MW;
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Pfam; PF01299; Lamp; 1.
PRINTS; PR00336; LYSASSOCTDMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001)
EMBL, AKO04637; BABB3428.1; -.
MGD; MGI:96745; Lamp1
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STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851;
                           Bacillus subtilis.
Bacteria, Firmicutes;
                                                                      YFMD protein.
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         NCBI_TaxID=1423;
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         Q9F1U5;
Q9F1U5;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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"Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region of the Bacillus subtilis genome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and a general stress response protein.";
Gene 194:191-199(1997).
EMBL; 299108; CAB1580.1; -.
EMBL; D86417; BAA22318.1; -.
InterPro; IPR000522; FecCD.
Pram; PF01032; FecCD.
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Complete proteome.
SEQUENCE 333 AA;
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7; Conserv
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(TremBLrel. 16, Created)
(TremBLrel. 16, Last sequence update)
(TremBLrel. 19, Last annotation updat
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01-MAY-2000 (TrEMBLrel. 13, La
01-MAR-2003 (TrEMBLrel. 23, La
Receptor-protein kinase-like p:
F26013.190.
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Q9SCZ4;
Q1-MAY-2000
01-MAY-2000
01-MAR-2003
                                                                                                                                     Pfam; PF00069; pkinase; I.

Prodom; PD000001; Prot kinase; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE ST; 1.
                                                                                                                                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
-:- SIMILARITY: BELONGS TO THE SER/THR FAMILY
EMBL; AL133452; CAB63019.1; -.
InterPro; IPR002799; Prot kinase.
InterPro; IPR002790; Ser thr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;

eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Delseny M., Berger
Lemcke K., Mayer K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cows with mastitis.";
Vet. Microbiol. 79:267-274(2001).
EMBL; AB043554; BAB18547.1; -.
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Hayakawa Y.;
"Variation of the agr locus in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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77.8%;
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Last annotation update)
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Pred. No. 1.2e
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Pred. No. 5.5,
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A Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,

A Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,

A Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E.,

A Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,

A Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,

B Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

"Fell Length cDNA of gene F26013.190/AT3951550 (GI:6572076).";

L Submitted (MAY-2001) to the EMEL/GenBank/DDBJ databases.

C. -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

N InterPro; IPR00071: PROTEIN KINASE.

N InterPro; IPR00279; Ser thr_pkinase.

Pfam; PF00066; pkinase; I.

N Pfam; PF00066; pkinase; I.

N PROSITE; PS00101; PROTEIN KINASE_DOM; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

N PROSITE; PS00101; PROTEIN_KINASE_ST; 1.

N PROSITE; PS00101; PROTEIN_KINASE_ST; 1.

N PROSITE; PS00101; PROTEIN_KINASE_TP; 1.
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01-NOV-1996
01-NOV-1996
01-MAR-2003
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01-DEC-2001 (TrEMBLrel. 29, Last sequence update)
01-DEC-2003 (TrEMBLrel. 29, Last sequence update)
01-MAR-2003 (TrEMBLrel. 29, Last annotation update)
Hypothetical 98.2 kDa protein.
Arabidopsis thallana (Mouse-ear cress).
Arabidopsis thallana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=K-12/K-1;
MEDLINE=92138601; PubMed=1735705;
Steenbergen S.M., Wrona T.J., Vimr E.R.;
"Functional analysis of the sialyltransferase coli KI and K92.";
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EMBL; M76370; AAA24214.1; -.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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          SEQUENCE FROM N.A.

STRAIN-NCTC 11168;

MEDLINE=20150912; PubMed=10688204;

MEDLINE=20150912; PubMed=10688204;

Parkhill J. Wren B.W. Mungall K. Ketley J.M., Chur Basham D., Chillingworth T., Davies R.M., Feltwell T. Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Pen Quail M.A., Rajandream M.A., Rutherford K.M., van Vli Whitehead S., Barrell B.G.; Rutherford K.M., van Vli Whitehead S., Barrell B.G.; Pallen M.J., reveals hypervariable sequences.";

Nature 403:665-668(2000).

EMBL; AL139078; CAB73837.1; -.
                                                                                                                                                                                                                                                                                       Q9PMP4;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gramene;
SEQUENCE
                                                                                                                                                                                                       CJ14130.
Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonp
Dacteria; Proferaceae; Campylobacter.
                                                                                                                                                                                                                                                             Possible CJ1413C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-2001) to the EMBL/GenBank/DDBJ EMBL; AP004231; BAB89223.1; -. EMBL; AP004232; BAB90716.1; -:
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STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group)
clone:0SJNBa0025J14 ";
Submitted (OCT-2001) to the EMBL/GenBanl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
05JNBa00260J14.9 protein (O5JNBa0051H17.31 protein).
OSJNBA0026J14.9 OR OSJNBA0051H17.31.
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ebrhartoideae; Oryzaae; Oryza.
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                  NCBI_TaxID=197;
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'-2000 (TrEMBLrel. 15, Last sequence update)
'-2001 (TrEMBLrel. 19, Last annotation update)
Le polysaccharide modification protein.
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Pred. No.
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                                                         Campylobacter jejuni
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Q8EV24;
Q8EV24;
01-MAR-2003 (TEMBLEEL 2
01-MAR-2003 (TEMBLEEL 2
01-MAR-2003 (TEMBLEEL 2
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01-NOV-1999
01-DEC-2001
                                                                                                                                                  MEDIINE=22354719; PubMed=12466555; Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri 'Sasaki Y., Ishikawa J., Yamashita R., Sasaki T., Hattori M., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M., "The complete genomic sequence of Mycoplasma penetrans, intracellular bacterial pathogen in humans."; Nucleic Acids Res. 30:5293-5300(2002).

EMBL, AP004173; BAC44537.1;
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EMBL; AF127177; AAD32184.1; -.
SEQUENCE 406 AA; 48449 MW; 99C
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Clarke B.R., Pearce R., Roberts I.S.;
"Genetic organization of the Escherichia coli K10 capsule gene
cluster: identification and characterization of two conserved regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma penetrans.
Bacteria; Firmicutes;
NCBI_TaxID=28227;
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SEQUENCE
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EMBL; AF085697; AAD42254.1; -.
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRALNEWVU-1853;
MEDLINE=201-1853; PubMed=10692167;
Noormohammadi A.H., Markham P.F., I
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                                                                                                                                                                          SEQUENCE FROM N.A.

STRALN=06:H1 / CFT073 / ATCC 700928;

MEDLINE=20388234; PubMed=12471157;

Melch R.A., Burland V., Plunkett G. III, Redford P., Rc
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
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US-09-882-835-2
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US-09-053-197A-8
US-09-053-197A-8
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ALIGNMENTS

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Jeavis, Richard P.

Ji, Guangyong

TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL

TITLE OF INVENTION: INTERFERENCE

FILE REFERENCE: 600-1-231N

CURRENT APPLICATION NUMBER: US/09/339,511

CURRENT FILING DATE: 1999-06-24

PRIOR FILING DATE: 1999-06-24

PRIOR FILING DATE: 1998-06-24

PRIOR FILING DATE: 1998-06-24

PRIOR FILING DATE: 1988-06-24

PRIOR FILING DATE: 1988-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide; NAME/KEY: VARIANT; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position. US-09-339-511-1
GENERAL INFORMATION:
APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE: 63753/7
CURRENT APPLICATION NUMBER: US/08/861,476C
CURRENT FILING DATE: 1997-05-22
                                                                                                                                              Sequence 3, Application Patent No. 6447786
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ORGANISM: Artificial Sequence
FEATURE:
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US-08-861-476C-6
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APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE: 63753/7
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PRIOR FILING DATE: 1998-06-24
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SOFTWARE:
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SOFTWARE: PatentIn Ver. 2.0
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tent No. 6337385
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                                          OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
OTHER INFORMATION: Xaa represents any
                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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Mayville, Patricia
No. 6337385ick, Richard
Beavis, Ronald
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Patent No. 6337385
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                                                                                                       APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
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TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
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TYPE: PRI
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LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at
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o. 6337385
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Mayville, Patricia
No. 6337385ick, Ri
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85ick, Richard P.
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l; Mismatches
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Best Local
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APPLICANT:
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                                                                                                                                                                Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ji, Guangyong
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: INTERFERENCE
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-221N
FILE REFERENCE: 600 CURRENT APPLICATION CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 8 SOFTWARE: PatentIn Ver. 2.0
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LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position
                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
NAME(KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (5)
OTHER INFORMATION: Xaa represents any
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                                         PPLICANT: Ji, Guangyong
ITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
ITLE OF INVENTION: INTERPERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                 INFORMATION
                                                                                                                                                              4, Application US/09339511
5. 6337385
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5. 6337385
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8; Conserv
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8; Conserv
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                                                                                                  Muir, Tom
Mayville, Patricia
No. 6337385ick, Richard
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No. 6337385ick, Richard
Beavis, Ronald
                                                                                       Beavis, Ronald
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                              600-1-231N
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              NUMBER: US/09/339,511
 1999-06-24
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Pred. No. 2
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2.5e+05;
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Best Local Similarity
Matches 8; Conserv:
                                                                                            US-09-882-835-2
                                                                                                          RESULT 10
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                                           Sequence 2, Applicat patent No. 6462187 GENERAL INFORMATION:
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LENGTH: 9
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SEQ ID NO 3
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Best Local
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Patent No. 6337385
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ji Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1399-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
SOFTMARE: Patentin Ver. 2.0
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APPLICANT: Bandaru, TITLE OF INVENTION: TITLE OF INVENTION:
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
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LOCATION: (5)
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Mayville, Patric:
No. 6337385ick, 1
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                                                                             Application US/09882835
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22109, A NOVEL HUMAN THIOREDOXIN FAMILY
MEMBER AND USES THEREOF
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Pred. No. 2.5e+05;
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RESULT 12
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; ORGANISM: Homo sapiens
US-09-882-835-2
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Best Local
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CURRENT APPLICATION NUMBER: US/09/882,835
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/211,673
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9567
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Fukuda, Minoru
TITLE OF INVENTION: CELL SURFACE LAMP EXPRESSION
TITLE OF INVENTION: SELECTIN-DEPENDENT ADHESION
NUMBER OF SEQUENCES: 18
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ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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nes 6; Conserv
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                                                                                                          263 GMNASSSRF 271
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amino acid
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Pred. No.
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Pred. No. 87;
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                                                                                                                                                                                                                                                                                                                                      DB 1; Length 353;
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US-08-186-833-2
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Patent No. 5646248
GENERAL INFORMATION:
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Best Local
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/073,807A
FILING DATE: 08-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
RESISTRATION NUMBER: 31.615
REFERENCE/DOCKET NUMBER: 31.515
REFERENCE/DOCKET NUMBER: 31.5367
TELECOMMUNICATION INFORMATION:
COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word, Version #5.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 18
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Tarczynski, Mit
APPLICANT: Jensen, Richard
APPLICANT: Bohnert, Hans J
TITLE OF INVENTION: Transg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
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APPLICANT: Lowe, John B.
APPLICANT: Fukuda, Minoru
                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                              STREET: P.U. -
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 GMNASSSRF 298
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California
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P.O. Box 2113, Fir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                               Jensen, Richard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.48;
                                                                                                                                                                                                                                                                                                        Transgenic Plants With Enhanced Mannitol
                                                                                                                                                                                                                             First Wisconsin Plaza
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Pred. No. 1e+02;
1; Mismatches
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REFERENCE/DOCKET NUMBER: 9221
TELECOMMUNICATION INFORMATION:
TELEPHON: (608) 251-906
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-186-833-2
                                                                              TELEFAX: 810-539-5055;
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
TOPOLOGY: linear
JOUGHOUSE BYOTHER
US-08-399-561-2
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,561
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
RECISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 9-305 (Hebrew Univ.)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 810-539-5050
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Best Local Similarity 75.0%;
Matches 6; Conservative
                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hirschberg, Joseph
APPLICANT: Cunningham Jr., Francis X.
APPLICANT: Gantt, Elisabeth
TITLE OF INVENTION: Lycopene Cyclase Gene
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800 PRIOR APPLICATION NUMBER:
y Match 74.4%; Score 29; DB 1; Local Similarity 75.0%; Pred. No. 1.1e+02; 1es 6; Conservative 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5792903thwestern Highway, Suite 410
CITY: Farmington Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 48334
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                                         Length 411;
  1; Indels
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Gaps
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Search completed: January 29, 2004, 15:03:20 Job time : 12.1176 secs

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                                                                                                                                                                                           NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMFUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TYPE: amino acid
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Patent No. 5646248
                                                                         Best Local Similarity
Matches 6; Conserv
                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/073,807A FILING DATE: 08-JUN-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CELL SURFACE LAMP EXPRESSION TITLE OF INVENTION: SELECTIN-DEPENDENT ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Diego
STATE: California
COUNTRY: United States
290 GMNASSSRF 298
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                                   1 GVNAXSSLF 9
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                                                                         74.4%;
ilarity 66.7%;
Conservative
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Lowe, John B
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                                                                                          Score 29; DB 1;
Pred. No. 1.1e+02;
                                                                           Mismatches
                                                                                                            Length 416;
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Title:
Perfect score:
Sequence:
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Maximum DB
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                                                                                                                                                                                                                                                                                Score
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Se Q
   protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
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length: 2000000000
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Match
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Gapop 10.0 ,
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd
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US-10-032-950-5
US-10-032-950-2
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ALIGNMENTS

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FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,95
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                        TYPE: PRT
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position
US-10-032-950-1
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Matches
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APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453A11ck, Richard P.
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
1 GVNAXSSLF 9
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1 GVNAXSSLF 9
                                                                                   Similarity 9; Conserv
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                                                                                94.9%; Score 37; DB
100.0%; Pred. No. 7e-
tive 0; Mismatches
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US-10-201-444-3

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US-10-201-444-3
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SEQ ID NO 6
LENGTH: 47
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APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S.
FILE REFERENCE: 63753/7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/10201444

publication No. US20030078378A1

GENERAL INFORMATION:

APPLICANT: New York University Medical Center

TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS

FILE REFERENCE: 63753/7

CURRENT APPLICATION NUMBER: US/10/201,444

CURRENT FILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: US/10/8/861,476

PRIOR FILING DATE: 1997-05-22
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CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US/08/861,476
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERPERENCE
                                                                                          APPLICANT: Muir,
APPLICANT: Mayv
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                                                       Mayville, Patricia
No. US20020077453Alick,
Beavis, Ronald
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Pred. No. 7e+(
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RESULT 6 US-10-032-950-2

Sequence 2, Application US/10032950 Publication No. US20020077453A1 GENERAL INFORMATION:

APPLICANT: Muir, Tom

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SEQ ID NO 6
LENGTH: 9
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description
OTHER.INFORMATION: peptide
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APPLICANT:
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Best Local (
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CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
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CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL TITLE OF INVENTION: INTERFERENCE FILE REFERENCE: 600-1-231N
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                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                         OTHER INFORMATION: Xaa represents any amino
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                  GVNAXSSLF 9
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No. US20020077453Alick,
Beavis, Ronald
GVNAXSALF 9
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                                                             Conservative
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88.9%;
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Pred. No.
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Pred. No. 7e+05;
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; OTHER INFORMATION: Xea represents any amino acid
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                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 9
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SEQ ID NO 2
LENGTH: 9
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FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
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                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT
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FEATURE:
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No. US20020077453Alick, Richard
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Pred. No. 7e+0
0; Mismatches
                                                                        Score 32; DB 13
Pred. No. 7e+05;
0; Mismatches
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7e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 130, Application US/10004378A Publication No. US20030228301A1 GENERAL INFORMATION:
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LENGTH: 9
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CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
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APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453Alick, Richard P.
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Li, Li
APPLICANT: Furtak, Kazarzyna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ji, GUANGYONG
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERPERENCE
FILE REFERENCE: 500-1-231N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequ
OTHER INFORMATION: peptide
NAMES/KEY: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION
T: Ellerman, Karen
T: Gangolli, Esha A
INVENTION: No. US20030228301A1el Human Proteins, Polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
8; Conser
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Tchernev, Velizar T
Vernet, Corrine A
Spytek, Kimberly A
                                                    Peyman, John A
Gunther, Erik
Stone, David J
                                                                                                          Lepley, Denise M
Gerlach, Valerie
Edinger, Schlomit
MacDougall, John R
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Shimkets, Richard
Guo, Xiaojia Sasha
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Grosse, William M
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Malyankar, Uriel M
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100.0%; Pred. No.
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1. 7e+05;
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  Encoding
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US-10-004-378A-131
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SEQ ID NO 130
LENGTH: 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 131, Application US/10004378A Publication No. US20030228301A1
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Matches 6; Conserv
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/243,622
PRIOR FILLING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/273,047
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/243,591
PRIOR FILING DATE: 2000-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,767
PRIOR FILING DATE: 2000-10-24
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PRIOR APPLICATION NUMBER: 60/242,789
PRIOR FILING DATE: 2000-10-24
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PRIOR APPLICATION NUMBER: 60/300,206
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                                           APPLICANT
                                                           APPLICANT:
                                                                                                                   APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 GVNLFSSIF 347
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Tchernev, Velizar T
Vernet, Corrine A
Spytek, Kimberly A
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                                                     Shenoy, Suresh G
Grosse, William M
Alsobrook II, John P
Lepley, Denise M
Gerlach, Valerie
Edinger, Schlomit
MacDougall, John R
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Casman, Stacie J
Burgess, Catherine E
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Shimkets, R
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Stone, David J
                   Peyman, John A
Gunther, Erik
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Pred. No.
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CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 191
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 131
LENGTH: 465
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-10-004-378A-131
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                                                                                               ; LENGTH: 465
TYPE: PRT
; ORGANIZM: Drosophila melanogaster.
US-10-108-605-227
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US-10-108-605-227
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; Publication No. US200;
; GENERAL INFORMATION:
; APPLICANT: Broadus;
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PRIOR FILLING DATE: 2000-10-24
PRIOR PELLING DATE: 2000-10-24
PRIOR PELLING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/243,622
PRIOR FILLING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/243,622
PRIOR APPLICATION NUMBER: 60/273,047
PRIOR APPLICATION NUMBER: 60/273,047
PRIOR APPLICATION NUMBER: 60/243,591
PRIOR APPLICATION NUMBER: 60/243,591
PRIOR APPLICATION NUMBER: 60/243,590
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/243,590
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
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Best Local S
Matches 6
Query Match
Best Local Similarity
Matches 6; Conserv
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CURRENT APPLICATION NUMBER: US/10/004,378A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/242,882
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/242,765
PRIOR FILLING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/300,206
PRIOR FILLING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/242,789
PRIOR FILLING DATE: 2000-10-24
PRIOR FILLING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Xim
APPLICANT: Kamdar, Xim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCOUTING OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
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o. US20020160934A1
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                          76.9%;
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Pred. No. 1.4e+02;
1; Mismatches 2
                          Score 30; I
Pred. No. 1
                          DB 14;
1.4e+02;
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, LENGTH: 633
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-10-369-493-6225
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                                                                               ; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any US-10-032-950-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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Query Match
Best Local Similarity
Matches 8; Conserv
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CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
EQ ID NO 3
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
FULR REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453A1ick, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         guence 3, Application US/10032950 blication No. US20020077453A1
                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT
                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 INAFSSLF 335
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    Conservative
                 74.4%;
88.9%;
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75.0%;
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Pred. No. 2e+02;
Score 29; DB 13
Pred. No. 7e+05;
0; Mismatches
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                                       DB 13; Length 9;
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; ORGANISM: Homo sapiens US-10-145-586-46
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TITLE OF INVENTION: Identification of Essent TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR PILING DATE: 2000-03-21

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/242,578

PRIOR PELING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/269,308
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46
LENGTH: 332
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: Alexandra Glucksmann, Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10385, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
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APPLICANT: Bandaru, Rajasekhar
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE.
TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY REFERENCE: 10488-188001
CURRENT APPLICATION NUMBER: US/10/145,586
CURRENT FILING DATE: 2002-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith V
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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Zyskind, Judith W.
Wall, Daniel
Wall, Daniel
Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/10145586
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66.78;
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Pred. No. 1.7e+02;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                    Essential
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; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE; FASTSEQ for Windows Version 4.0
; SEQ ID NO 10385
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10385

Query Match
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Oy 1 GVNAXSSL 8

Oy 1 GVNAXSSL 8

Search completed: January 29, 2004, 15:01:44

Job time: 25.5441 secs
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Run on:

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Minimum DB seq
Maximum DB seq
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Perfect score:
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2: /SIDS1/gcgdata/gei
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Maximum Match
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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd
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                                           S. aureus peptide Cyclic peptide SEQ AgrD-autoinducing Staphylococcus aur Staphylococcus aur Protected peptide
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ALIGNMENTS

Staphylococcus aureus infection; cyclic peptide; AgrD; agr response; virulence factor; treatment. S. aureus peptide #2 used for bacterial interference (UYRQ) UNIV ROCKEFELLER. (first entry) aureus 98US-0103438 99WO-US14562 5 /label= Unknown Location/Qualifiers /note= peptide; "N-terminal residue forms bond with C-terminal residue to form a cyclic peptide" ø ያ

Result

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RESULT 2
ABP53541
ID ABP5
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Best Local S
Matches
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                                                                                                                                 24-JUN-1998;
24-JUN-1999;
                                                                                                                                                                                                                                                                                                                              ABP53541;
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 Claim
                        New cyclic
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(MAYV/)
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(JIGG/)
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                                           WPI; 2002-681366/73
                                                             Muir TW,
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                 infections
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) MAYVILLE P.
) NOVICK R P.
) BEAVIS R.
) JI G.
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Page
                                                            Mayville P,
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 10;
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99US-0339511
                                                                                                                                                                                                                              Location/Qualifiers
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English
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The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is a secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. Preferred peptides may have the sequence NH2-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z residue and COOH other than a thioester
                                                                                                                                                                                                      Claim 7;
                                                                                                                                                                                                                                                                  Novel synthetic, interference and
                                                                                                                                                                                                                                                                                                                                   WPI; 2002-170774/22
                                                                                                                                                                                                                                                                                                                                                                             Muir TW,
                                                                                                                                                                                                                                                                                                                                                                                                                     (UYRQ )
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bond, where X is an amino acid, an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The cyclic bond is especially a lactam or lactone bond. The thiololactone structure within native AgrD peptides is required for activation of the agr response. Elimination of the thiol ester component of the cyclic ring structure can destroy agr response activating activity while preserving and enhancing inhibitory activity. A claimed method of preparing a cyclic peptide resin support; a linear peptide chain on to a solid phase resin support; deprotecting the resulting protected assembled peptide; treating the deprotected peptide with neutral buffer for a time sufficient to form the cyclic peptide and cleave the peptide is useful for and recovering the cyclic peptide. The peptide is useful for infection
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          This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
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cexample of the preparation of novel synthetic cyclic peptides of the invention (see AAM50899-906). The peptide corresponds to the CC (lactone). It was synthesised on a Wang-resin using an Fmoc (lactone). It was synthesised on a Wang-resin using an Fmoc (was cleaved from the support and the Ser-5 residue deprotected by treatment with a trifluoroacetic acid:anisole:water mixture (90:5.5) for 4 hr. The partially protected peptide-alpha (90:5.5) for 4 hr. The remaining protecting groups were then complete after 2 hr. The remaining protecting groups were then complete after 2 hr. The remaining protecting groups were then complete after 2 hr. The remaining protecting groups were then complete after 2 hr. The remaining protecting the agr response of the cyclic peptide is capable of inhibiting the agr response of Replacement of the thiololactone structure within native Agr peptides is required for activation of this response. Replacement of the thiololactone structure within response activating activity while preserving and confection inhibitory activity. The cyclic peptides are useful for affection in the persent case of a saureus of the cyclic peptides are useful for affection.
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Query Match Best Local Similarity

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GANAXSSLF

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                                                                                   thioster peptide. The peptide is derived from the cyclic AgrD2 competition of Staphylococcus aureus group II. AgrD2 is a secreted carried encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrD3 promoter. This allowed activation or inhibition of the agrD3 promoter. This allowed activation or inhibition of the agrD3 promoter to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone cyclic peptide (see AAMS1001), the present peptide was unable to either activate or inhibit the agr response, even when added to cultured cells at uM concentrations. The invention provides claimed cyclic peptides (see AAMS1099-906 and AAMS1099) and methods for preparing them. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-170774/22
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RESULT 9
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                                                                                                                                           Query Match
Best Local
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AAM51004 standard; Peptide; 9 AA
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Synthetic.
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77.8%;
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Pred. No. 9.3e+05;
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RESULT 10

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                                                                                                                               the agrP3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. The lactone AgrD2 peptide inhibited the agr response of group I S. aureus strains without activating the agr response in group I, II or III strains. The invention provides claimed cyclic peptides (see AAM50899-906 and AAM50899) and methods for preparing them, especially peptides where the cyclic bond is a lactom or lactone bond. The cyclic peptides are useful for bacterial interference especially for the treatment of S. aureus infection.
                                                                                                                                                                                                                                                                                                          The present sequence is that of a novel synthetic AgrD2 lactone cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactone bond. The peptide is derived from an AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrP3 promoter. This allowed activation or inhibition of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stpahylococcus Synthetic.
                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AgrD2; agr
infection;
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  Similarity 7; Conserv
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  Conservative
                                                                                         AA;
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/note= "note linked
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                     87.2%;
77.8%;
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Score 34; DB 23; : Pred. No. 9.3e+05; 0; Mismatches 2;
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RESULT 11
AAY67851
ID AAY67857
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Best Local :
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                                                                                                                                                                                                                                                                                                                                           The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Synergistic antiblotic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2000; 2000US-203000P.
07-DEC-2000; 2000US-254398P.
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                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 33; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of autoinducer-2 agonists or antagonists autoinducer-2 receptor, regulating bacterial also antibiotic compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide-mediated quorum sensing inhibitor peptide cyclo-XII
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Staphylococcus
                           S. aureus peptide #1 used for bacterial interference.
                                                         25-APR-2000
                                                                                    AAY67851;
                                                                                                                AAY67851 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                quorum sensing.
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) QUOREX PHARM IN
) UNIV TECHNOLOGI
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                                                                                                                                                                                       GVNASSSLF
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                                                         (first
   aureus
                                                                                                                                                                                       Q
                                                       entry)
                                                                                                                                                                                                                                                           87.2%;
77.8%;
   infection;
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                                                                                                                                                                                                                                             Score 34; DB 23;
Pred. No. 9.3e+05;
0; Mismatches 2
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; accessory gene regulator; cyc
cyclic peptide; AgrD; agr response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shokat K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for regulating activity growth and pathogenesis,
                                                                                                                                                                                                                                                                          Length 9;
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RESULT 12
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AC AAy67
AC AAy67
AC Staph
CF Staph
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XX Staph
XX Wisc-
FT Misc-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a cyclic peptide derived from the Staphylococcus aureus AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muir TW, Mayville P,
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                                                                                                                                                                         Key
Misc-difference
                                                                                                                                                                                                                                                                                                               Staphylococcus aureus infection; AgrD; virulence factor.
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  24-JUN-1999;
                                                       29-DEC-1999.
                                                                                                       W09967286-A2
                                                                                                                                                                                                                                                                Staphylococcus aureus
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8; Conserv
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     99WO-US14562
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/label= Unknown
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Pred. No.
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RESULT 13
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Matches 8
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(BEAV/)
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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24-JUN-1999;
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WPI; 2002-681366/73
                 Muir TW,
                                                                                                                 27-DEC-2001; 2001US-0032950
                                                                                                                                   20-JUN-2002
                                                                                                                                                                                                                         agr response
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                                 MUIR T W.
MAYVILLE
NOVICK R
BEAVIS R.
JI G.
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8; Conserv
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                Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                          9 AA;
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NEW YORK STATE.
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                                                                                                                                                                           Location/Qualifiers
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Pred. No. 9.3e+05;
0; Mismatches 1
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                  Beavis R,
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ARESULT 14
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention. The present invention also describes a method for treating Staphylococcus aureus infection comprising the administration of a composition comprising (I). (I) has antibacterial activity, and can be used as an agr gene response inhibitor. The peptides are useful for treating S. aureus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus antibacterial;
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The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response (Staphylococcus aureus. It is an AgrD-autoinducing peptide, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page 10;
                                                                           Claim 7;
                                                                                                                                      Novel synthetic, interference and
                                                                                                                                                                                               WPI; 2002-170774/22.
                                                                                                                                                                                                                                       Muir TW,
                                                                                                                                                                                                                                                                                                                                      24-JUN-1998;
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NEW YORK STATE.
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infection; therapy; cyclic.
                                                                                                                                                                                                                                                                                                                                                                              9908-0339511
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                                                                                                                                    cyclic AgrD-autoinducing peptide for bacterial for treating Staphylococcus aureus infection i
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                                                                                                                                                                                                                                       Novick
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Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 structure within native AgrD peptides is required for activation of the agr response. Elimination of the thiol ester component of the cyclic ring structure can destroy agr response activating activity while preserving and enhancing inhibitory activity. A claimed method of preparing a cyclic peptide involves; assembling a linear peptide chain on to a solid phase resin support; deprotecting the resulting protected assembled peptide; treating the deprotected with neutral buffer for a time sufficient to form the cyclic peptide and cleave the peptide from the support; and recovering the cyclic peptide. The peptide is useful for bacterial interference, especially for the treatment of S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgrD is a secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. Preferred peptides may have the sequence NHZ-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z residue and COOH other than a thioester bond, where X is an amino acid, an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The cyclic bond is especially a lactam or lactone bond. The thiololactone
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                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
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The present sequence is that of a protected peptide used in an accessing an example of the preparation of novel synthetic cyclic peptides of the invention (see AAM50899-906). The peptide corresponds to the Staphylococcus aureus AgrDII sequence with a Cys to diaminopropionic acid (Ipr) mutation (lactam). It was synthesised on a Wang-resin cusing an Fmoc N-alpha protection strategy. Following chain assembly, the peptide was cleaved from the support and the Dpr-5 residue deprotected by treatment with a trifluoroacetic acid, anisole; water mixture (90:5:5) for 4 hr. The partially protected peptide-alpha carboxylates were then dissolved in DMF and treated with PMDP.

Cyclization was complete after 2 hr. The remaining protecting groups were removed by treatment with HF and the peptide purified by HPPC. The cyclic peptide is capable of inhibiting the agr response of staphylococcus aureus. The thiololactone structure within native Replacement of the thiol ester component of the cyclic ring structure with a lactam (as in the present case) or a lactone can can be component of the cyclic ring enhancing inhibitory activity. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus of the cyclic peptides are useful for the cyclic peptides.
    Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
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N,Alternate names: avian knotted-related protein; homeotic protein AKR

C,Species: Gallus gallus (chicken)

C,Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999

C,Accession: S58439; S58440

R,Ryan, A.K.; Tejada, M.L.; May, D.L.; Dubaova, M.; Deeley, R.G.

submitted to the EMBL Data Library, April 1995

A,Description: Isolation and characterization of the chicken homeodomain protein AKR.
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A;Accession: S58439
A;Molecule type: mRNA
A;Residues: 1-269 <RYA>
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Best Local S
Matches 7
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A37361	T02146	A81343	S48463	T41402	B85398	T05210	G96713	T24127	S57097	871307	AD0105	A84187	\$64931	D85978	A98133
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ALIGNMENTS

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RESULT 2
A28067
A280667
LYPOSOMBL Membrane glycoprotein LAMP-1 - mouse
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Apecies: Mos musculus (house mouse)
C;Apecies: N. J. 28067
R;Chen, J.W.; Cha, Y.; Yuksel, K.U.; Gracy, R.W.; August, J.T.
J. Biol. Chem. 263, 8754-8758, 1988
A;Title: Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycopr
A;Reference number: A28067; MUID:88243732; PMID:3379044
A;Accession: A28067
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: negative regulator of apoVLDLII (major egg yolk apolipoprotein) A;Note: expressed in liver during early embryogenesis and in non-hepatic adult C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;36-95/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: EMBL:U25353; NID:g857681; PIDN:AAA83567.1; PID:g857682 R;Ryan, A.K.; Tejada, M.L.; May, D.L.; Dubaova, M.; Deeley, R.G. Nucleic Acids Res. 23, 3252-3259, 1995 A;Title: Isolation and characterization of the chicken homeodomain protein AKR. A,Teference number: S58440; MUID:95396587; PMID:7667102 A,Accession: S58440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 35-94 <RYF>
A;Cross-references: EMBL:U25353
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120K lysosomal membrane glycoprotein precursor NALternate names: sialoglycoprotein C;Species: Rattus norvegicus (Norway rat) C;Date: 18-Oct-1989 #sequence_revision 30-Sep-C;Accession: A30200; S03331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P2B/LAMP-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr.1993 #sequence_revision 17-Apr.1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:J03881; NID:g198706; PIDN:AAA39411.1; PID:g293692 A;Note: the authors translated the codon Aff for residue 1 as Leu and CCG C;Superfantly: lysosome-associated membrane protein C;Keywords: glycoprotein; membrane protein
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A;Cross-refe
                                                                                          A; Molecule type: mRNA
A; Restdues: 22-407 <HIM>
A; Cross-references: EMBL: X14765; NID: 956577; PIDN: CAA32873.1;
A; Note: part of this sequence, including the amino end of the
                                                                                                                                                 A,Title: Isolation and sequencing of a cDNA clone encoding A;Reference number: S03331; MUID:89153580; PMID:2920835 A;Accession: S03331
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A;Reference nu
                                                                                                                                                                                                                                                                                                                 R;Howe, C.L.; Granger, B.L.; Hull, M.; Green, S.A.; Gabel, C.A.; Helenius, A.; Proc. Natl. Acad. Sci. U.S.A. 85, 7577-7581, 1988
A;Title: Derived protein sequence, oligosaccharides, and membrane insertion of
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A,Note: the authors translated the codon GGG f.
R,Håneno, M, Nogucchi, Y, Sasski, H., Tanaka,
FEBS Lett 244, 351-356, 1989
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A; Residues: 1-407 < HOW>
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                                                   Superfamily: lysosome-associated membrane protein;Keywords: glycoprotein; membrane protein
22-407/Product: lysosomal membrane glycoprotein, 107K #status;
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AgrD protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: C89995
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
Ra, Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                A;Molecule type: protein
A;Molecule type: protein
A;Residues: 'T',16-40',R',42-46 <COC>
A;Residues: 'T',16-40',R',42-46 <COC>
C;Superfamily: mitochondrial processing peptidase alpha chain
C;Superfamily: mitochondrial matrix; mitochondrion; oxidative phosphorylatio:
C;Superfamily: transit peptide (mitochondrion) #status prodeicted <TNP>
F;1-14/Domain: transit peptide (mitochondrion) #status prodein II #status experiment
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A; Residues: 1-453 <GBN.
A; Cross-references: GB:X59693; NID:g299; PIDN:CAA42214.1; PID:g300
A; Cross-references: GB:X59693; NID:g299; PIDN:CAA42214.1; PID:g300
A; Note: part of this sequence, including the amino end of the mature
A; Note: part of this sequence, including the amino end of the mature
B; Cocco, T.; Lorusso, M.; Sardanelli, A.M.; Minuto, M.; Ronchi, S.; T
Bur. J. Biochem. 195, 731-734, 1991
By Title: Structural and functional characteristics of polypeptide sub
A; Reference number: S14093; MUID:91153313; PMID:1847870
A; Accession: S14093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II C;Species: Bos primigenius taurus (cattle) C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change C;Accession: S1621; S14093 R;Gencic, S.; Schaagger, H.; von Jagow, G. Eur. J. Biochem. 199, 123-131, 1991 Eur. J. Biochem. 199, 123-131, 1991
                                                                                                                                                                                     F;1-14/Domain: transit peptide (mitochondrion) \#stients;15-453/Product: ubiquinol-cytochrome-c reductase
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A;Accession: S16221
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A;Experimental source: strain N315
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A; Residues: 1-47 < KUR>
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hypothetical protein - Synechocystis sp. (strain PCC 6803)
C.Species: Synechocystis sp.
A; Variety: PCC 6803
C.Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C.Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C.Accession: S76294
R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, B.; Nakamura, Y.; Miyajima, N.; Co, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                 C;Geneti
A;Start
C;Superf
                                             hypothetical protein T16L1.300 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (;species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999 C;Accession: T04998 R;Bevan, M.; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hoheisel, J.; submitted to the Protein Sequence Database, November 1998
                                                                                                                                                 RESULT 9
T04998
                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:D64000;
A;Note: the nucleotide sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-340 < KAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-573 < PAR >
A;Reference number: Z15393
A;Accession: T04998
A;Molecule type: DNA
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Pred. No. 14;
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Pred. No. 14;
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multidrug resistance protein 1 homolog - barley C;Species: Hordeum vulgare (barley) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change C;Accession: T06165 R;Davies, T.G.E.; Theodoulou, F.L.; Hallahan, D.L.; Forde, B.G. Gene 199, 195-202, 1997 A;Title: Cloning and characterization of a novel P-glycoprotein A;Reference number: 215500; MUID:98019088; PMID:9358056
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A; Introns: 54/1; 117/3;
A; Note: T16L1.300
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A; Experimental source: cultivar Columbia;
                                                                                                                                                                                         .; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83144
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, F.; Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-1232 <DAV>
A;Residues: 1-1232 <DAV>
A;Cross-references: EMBL:Y10099; NID:g2292906; PIDN:CAA71179.1; PID:g229291
A;Experimental source: cv. Maris Mink
C;Superfamily: multidrug resistance protein; ATP-binding cassette homology
F;381-575/Domain: ATP-binding cassette homology <ABC>
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A;Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                  C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein PA4017 [imported] - C;Species: Pseudomonas aeruginosa
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A;Accession: T06165
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                   A;Molecule type: DNA
A;Residues: 1-213 <STO>
A;Cross-references: GB.AE004818; GB:AE004091; NID:g9950200; PIDN:AAG07404.1;
A;Experimental source: strain PAO1
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116

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GANAXSSLF

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R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 199
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84428
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Best Local Similarity
Marches 6; Conserv
                 C;Accession: C69812

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber S.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID;99069613; PMID;9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: C89103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein C18B10.10 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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C;Species: Arabidopsis thaliana (mouse-ear oress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H84428
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A;Molecule type: DNA
A;Residues: 1-250 <STO>
A;Cross_references: GB:F
                                                                                                                               ferrichrome ABC transporter (permease) homolog yfmD - Bacillus subtilis C;Species: Bacillus subtilis C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
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A;Residues: 1-291 <STO>
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Gene: C18B10.10
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Search completed: January 29, Job time: 12.1176 secs

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A;Reference number: Z23013
A;Accession: T45786
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-895 <DEL>
A;Cross-references: EMBL:AL133452
A;Experimental source: cultivar Coll
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A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor-protein kinase-like protein - Arabidopsis thaliana N;Alternate names: protein F26013.190 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000 C;Accession: T45-786 R;Delseny, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, December 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-333 <KUN>
A;Residues: 1-333 <KUN>
A;Cross-references: GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12580.1; PID:g26330
A:Exmerimental source: strain 168
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A;Note: F26013.190
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homes.
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A;Gene: yfmD
C;Superfamily: ferrichrome ABC transporter
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  SUMMARIES
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p59675 shigella fl
p49129 cricetulus
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p40490 drosophila
p25571 saccharomyc
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p40437 zea mays (m
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ALIGNMENTS

א ע	Mat	Ю H ∑					a a t a	Z P O X Q FI	E E M O O O A S	1 2 5
1 GANAXSSLF 9 222 GANAQSGLF 230	Query Match 84.6%; Score 33; DB 1; Length 269; Best Local Similarity 77.8%; Pred. No. 1.8; Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	NUCLEAI DIOCEII. DNA BIND 35 97 HOMEOBOX (TALE-TYPE). SEQÜENCE 269 AA; 29442 MW; 1074355DCC0C2253 CRC64;	P (353; AAA83567.1; 359; S58439. 1PR001356; Homeobox. 0046; homeobox; 1. 00400; Homeobox; 1.	wen the Swiss Institute of Bic wropean Bioinformatics Institu by mon-profit institutions a ied and this statement is not ies requires a license agreement in an email to license@isb-sin	LOCATION: Nuclear LOCATION: Nuclear BELONGS TO THE TALE/TGIF HOMEOBOX FAMILY. Contains 1 homeobox domain.	AKR."; Nucleic Acids Res. 23:3252-3259(1995). Nucleic Acids Res. 23:3252-3259(1995)!- FUNCTION: BINDS TO THE F' ELEMENT OF THE APOVLDUII GENE AND REPRESS ITS TRANSCRIPTION.	(1) SEQUENCE FROM N.A. TISSUE=Liver; MEDLINE=5396587; PubMed=7667102; Ryan A.K., Tejada M.L., May D.L., Dubaova M., Deeley R.G.; "Isolation and characterization of the chicken homeodomain protein	(Rel. 41, Last annotation upd protein AKR (Avian knotted-re is (Chicken). letazoa; Chordata; Craniata; V Aves; Neognathae; Galliforme	CHICK AKR CHICK STANDARD; PRT; 269 AA. Q90655; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update)

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RESULT 2
  EMBL; M32015; AAA39428.1; -.
EMBL; M25244; AAA39869.1; -.
EMBL; J03881; AAA39411.1; -.
PIR; A28067; A28067.
PIR; A28067; A28067.
PIR; A60534; A60534.
MGD; MGI:96745; Lamp1.
InterPro; IPR002000; Lamp.
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J. Biol. Chem. 265:7419-7423 (1990).

I- FUNCTION: PRESENTS CARBOHYDRATE LIGANDS

IMPLICATED IN TUMOR CELL METASTASIS.

ISUBCELLULAR LOCATION: Type I membrane pr

THIS PROTEIN SHUTTHES EPTATORIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 25-406 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=88243732; PubMed=379044;
Chen J.W., Cha Y., Yuksel K.U., Gracy R.W., August J.T.,
"Isolation and sequencing of a cDNA clone encoding lysosomal
glycoprotein mouse LAMP-1. Sequence similarity to proteins be
onco-differentiation antigens.",
J. Biol. Chem. 263:8754-8758(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Heffernan M., Yousefi
Submitted (FEB-1990) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization and cloning of lgp110, glycoprotein from mouse and rat cells."; J. Biol. Chem. 265:12036-12043(1990).
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911438; Q62020;
01-CCT-1989 (Rel. 12, Created)
01-NUG-1990 (Rel. 15, Last sequence update)
01-NVO-1997 (Rel. 35, Last annotation update)
Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1)
(LGP-120) (CD107A) (P2B).
LAMP1 OR LAMP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outest the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90237040; PubMed=2332434; Arterburn L.M., Earles B.J., August "The disulfide structure of mouse 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
Pfam; PF01299; Lamp; 1.

PRINTG; PR00336; LYSASOCTDMP.

PROSTTE; PR00310; LAMP 1; 2.

PROSITE; PS00311; LAMP_2; 1.

PROSITE: PROSITE ASSOCIATION OF THE PROSITE AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEMBRANE.

- PTM: O- AND N-GLYCOSYLATED; SOME OF THE N-GLYCANS ATTACHED LAMP-1 ARE POLYLACTOSAMINOGLYCANS (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE LAMP FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELLULAR LOCATION: Type I membrane protein.
PROTEIN SHUTTLES BETWEEN LYSOSOMES, ENDOS
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Rodentia;
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to the EMBL/GenBank/DDBJ databases
  LYSOSOME-ASSOCIATED
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(See http://www.isb-sib.ch/announce/
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  GLYCOPROTEIN
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P14562; P97620;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
1.vsosome-associated membrane glycoprotein | precursor (LAMP-1)
1.vsosome-associated membrane glycoprotein) (LGP-120) (CD107A).
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SEQUENCE OF 22-407 FROM N.A. MEDLLINE=89153580; PubMed=29208 Himeno M., Noguchi Y., Sasaki Sakaki Y., Kato K.; "Isolation and sequencing of a
                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
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                                                                 "Derived protein sequence, oligosaccharides, and membrane inserti
of the 120-kDa lysosomal membrane glycoprotein (lgp120):
identification of a highly conserved family of lysosomal membrane
                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Proc. Natl. Acad.
                                                                                                            SEQUENCE FROM N.A. MEDLINE=89017240;
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sequencing of a cDNA
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PubMed=2920835;
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r B.L., Hull M.,
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Pred. No. 2
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LF -> IP (IN REF. 3).
V -> I (IN REF. 2 AND 3).
C1BD373548BB9655 CRC64;
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CYTOPLASMIC (POTENTIAL)
FIRST LUMENAL DOMAIN.
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SECOND LUMENAL DOMAIN
                                                    85:7577-7581(1988)
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                 Tanaka Y., Furuno K.,
clone encoding 107 kDa
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EMBL; X14765; CAA32873.1; -.
EMBL; U75406; AAB19108.1; -.
PIR; A30200; A30200.
InterPro; IPR002000; Lamp.
Pfam; PF01299; Lamp; 1.
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STRAIN=Wistar Kyoto; TISSUE-AAOrtic smooth muscle;
Adams L.A., Werny I., Schwartz S.M.;
Submitted (CCT-1996) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: PRESENTS CARBOHYDRATE LIGANDS TO SELECTINS.
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PROSITE; PS00311; LAMP_2; 1.
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FEBS Lett. 244:351-356(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMPLICATED IN TUMOR CELL METASTASIS.
SUBCELLULAR LOCATION: Type I membrane protein.
THIS PROTEIN SHUTTLES BETWEEN LYSOSOMES, ENDOS
. Similarity
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                                    Glycoprotein; Lysosome; Signal.
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Score 33; DB Pred. No. 2.8; 0; Mismatches
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CYTOPLASMIC (P
FIRST LUMENAL
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                                    -> T (IN REF. 3).
D -> VT (IN REF. 3
25947490749A7C88
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Indels
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UCR2_BOVIN
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AC P33004;
DT 01-AUG-1991
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DT 12-FEB-2003
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RT Cloning of Nammalla, be
RT CLONING OF NAMMALLAND
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Mammalia; Eutheria;
Bovidae; Bovinae; Bo
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01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ubiquinol-cytochrome C reductase complex core protein
precursor (EC 1.10.2.2) (Complex III subunit II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88298703; pubMed=2841307;
Capaldi R.A., Gonzalez-Halphen D.,
"Complexity and tissue specificity
Chain.";
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98316377; PubMed=9651245;
Iwata S., Lee J.W., Okada K., Lee J.K.,
Link T.A., Ramaswamy S., Jap B.K.;
"Complete structure of the 11-subunit bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
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Gonzalez-Halphen D., Lindorfer M.A.,
"Subunit arrangement in beef heart c
Biochemistry 27:7021-7031(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cloning of bov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gencic S., Schaegger H., von Jagow G.;
"Core I protein of bovine ubiquinol-oytein-processing family.
additional member of the mitochondrial-protein-processing family.
Cloning of bovine core I and core II cDNAs and primary structure of
                                                                                                                                                                                                                                                                                                                                                                                   bc1 complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitochondria."
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Deisenhofer J.
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MEDLINE=97349328; PubMed=9204897;
Xia D., Yu C.A., Kim H., Xia J.Z., Kac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem. 199:123-131(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 15-43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bicenerg.
ferrocytochrome c.
SUBUNIT: BC1 COMPLEX CONTAINS 11 SUBUNITS; 3 RESPIRA
SUBUNIT: BC1 COMPLEX CONTAINS 11 SUBUNITS; 3 RESPIRA
(CYTOCHROME B, CYTOCHROME C1, RIESKE PROTEIN), 2 COI
6 LOW-MOLECULAR WEIGHT PROTEINS.
SUBCELLULAR LOCATION: Mitochondrial inner membrane;
SUBCELLULAR LOCATION: Mitochondrial inner membrane;
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16.
CAUTION: DOES NOT SEEM TO HAVE A PROTEASE ACTIVITY A
ZINC-BINDING SITE.
                                                                                                                                                                                                                   ence 281:64-71(1998).
FUNCTION: THIS IS A COMPONENT OF THE UBIQUINOL-CYTOCHROME C
REDUCTASE COMPLEX (III OR CYTOCHROME B-C1 COMPLEX), WHICH
IS PART OF THE MITOCHONDRIAL RESPIRATORY CHAIN. THE CORE PROTEIN
2 IS REQUIRED FOR THE ASSEMBLY OF THE COMPLEX.
CATALYTIC ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281
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e mitochondrial respiratory
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                                                                                                                                           RESPIRATORY SUBUNITS
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                                     IT LACK THE
                                                                                                                                                                                                                                                                                                                                                                                                                   cytochrome
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MEROPS; M16,974; -. MIC.974; -. MEROPS; M16,974; -. MIC.974; -. MIC.974; -. MIC.974; -. MIC.974; -. MIC.974; -. MIC.974; -. MIC.975; Peptidase_M16; 1. Pfam; PF0675; Peptidase_M16; 1. Pfam; PF05193; Peptidase_M16; 1. PROSITE; PS00143; INSULINASE; 1. PROSITE; PS00143; INSULINASE; 1. MITOCHONDRION.

Oxidoreductase; Transit peptide; 3D-structure.

OXIdoreductase; Transit peptide; 3D-structure.

MITOCHONDRION.

MITOCHONDRION.

TRANSITY

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                                                                                                                                                                                                                                                                                                                      EMBL; X59693; CAA42214.1;
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23-FEB-99.
 UBIQUINOL-CYTOCHROME C
CORE PROTEIN 2.
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Best Local &
Matches
EMBL; AE005181; AAG54345.1; -. EMBL; AE002550; BAB33468.1; -. .

PIR; E85485; E85485.

PIR; E90634; E90634.

HAMAP; MF_01056; -; 1.

InterPro; IRR001308; ETF_alpha.

PROSITE; PS00696; ETF_ALPHA; 1.

PROSITE; PS00696; FTAVOPTOTEIN; FA
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Q8XA27;
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HELIX
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhaw G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoy;
Hayashi T., Makino E., Ohnishi M., Murata T., Tanaka M., Tobe 'I'lda T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasuna;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatisthe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: Required for anaerobic carnitine reduction. May bring reductant to caiA (By similarity).
-!- PATHWAY: Carnitine metabolism (conversion of carnitine to gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gamman
Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FixB protein.
FIXB OR Z0048 OR ECS0045.
Escherichia coli 0157:H7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                butyrobetaine).
SUBUNIT: Heterodimer of fixA and fixB (By similarity)
SIMILARITY: BELONGS TO THE ETF ALPHA-SUBUNIT / FIXB F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 GSNATSSLY 310
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453 AA;
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Rel. 42,
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Pred. No.
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Tobe T.,
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RESULT 6
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Matches 5
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MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., S. Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R., "Extensive mosaic structure revealed by the complete genome of uropathogenic Sscherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plunkett G. III;
Unpublished observations (APR-2003).
-I- FUNCTION: Required for anaerobic
reductant to caiA (By similarity)
-I- PATHWAY: Carnitine metabolism (co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli Of.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FixB
                                                                                                                                                                     Electron transport;
NP_BIND 255
SEQUENCE 313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=06:H1 / CFT
                                                                                                                                                                                                                       EMBL; AE016755; -; NOT_ANNOTATED_CDS.
HAMAP; MF_01056; -; 1.
PROSITE; PS00696; ETF_ALPHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                                                                                                    butyrobetaine).
SUBUNIT: Heterodimer of fixA and fixB (By similarity).
SUBUNIT: Heterodimer of fixA and fixB (By similarity).
SIMILARITY: BELONGS TO THE ETF ALPHA-SUBUNIT / FIXB FAMILY.
SIMILARITY: BELONGS TO THE ETF ALPHA-SUBUNIT / FIXB FAMILY.
CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the third base of CAUTION: When this sequence was assembled, the control of the caution o
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OR C0051/C0052.
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Similarity 55.6%;
5; Conservative
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5; Conser
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33512 MW;
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                                                                                                                                                                   Flavoprotein; FAD; Complete proteome
283 FAD (ADP PART) (POTENTIAL).
33512 MW; A960554200E4D14D CRC64;
                                                                                                                       74.48;
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Pred. No.
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Pred. No.
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                                                                                                                       DB
19;
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                                                                                                       2.
                                                                                                                                      Length 313;
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Nuc.--
[3]
[3]
[3]
SEQUENCE FROM N.A.,
STRAINEK12 / MG1655;
STRAINEK12 / PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
Matther F.R., Plunkett G. III, Bloch C.A.,
Plattner F.R., Plunkett G. III, Bloch C.A.,
Collado-Vides J., Glasner J.D., Rc
N.W., Kirkpatrick H.A., Go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gregor J., Davidade B., Shao Y.;
Mau B., Shao Y.;
"The complete genome sequence of chience 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                               PubMed=12081978;

Walt A., Kahn M.L.;

WThe fixA and fixB genes are necessary for reduction in Escherichia coli.;

J. Bacteriol. 184:4044-4047(2002).

-i- FUNCTION: Required for anaerobic carr reductant to caiA.

-i- PANTHWAY: Carnitine metabolism (conver
EMBL; X71977; CAA50798 1;
EMBL; D10443; -; NOT ANNOT
EMBL; AB000114; AA673153.1
PIR; B64725; B64725.
HSSP; D38974; 1EFP.
HAMAP; MF 01056; -; 1.
EcoGene; EG11563; fixB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993
01-OCT-1996
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yura T., Mori H., Nagal H., Mayara I., Isono K., Mizobuchi K., Nakata A.;
"Systematic sequencing of the Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96066354; PubMed=7473063;
Eichher K., Buchet A., Bourgis F., Kleber
Mandrand-Berthelot M.-A.;
"The fix Escherichia coli region contains
carnitine metabolism.";
                                                                                                                                    This SWISS-PROT entry is copyright. It is produce the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as imodified and this statement is not removed. Use entities requires a license agreement (See http or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92334977; PubMed=1630901;
Yura T., Mori H., Nagai H., Nagata T.,
Isono K., Mizobuchi K., Nakata A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gamma;
Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FixB protein. FIXB OR B0042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=K12 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Basic Microbiol.
                                                                                                                                                                                                                                                                                   butyrobetaine).
SUBUNIT: Heterodimer of fixA and fixB (Probable)
SIMILARITY: BELONGS TO THE ETF ALPHA-SUBUNIT / F
CAUTION: Ref.2 sequence differs from that shown
                                                                                                                                                                                                                                                                              frameshifts.
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4 C
7 C
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annotation
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                                                                                                                                                                                                                                                                                                                                                                                                      carnitine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.A., Perna N.T., Burland V.D., Rode C.K., Mayhew G.F., A., Goeden M.A., Rose D.J.,
                                                                                                                                                        Noved. Usage by and for (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
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genome: analysis

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FIXB_SHIFL
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Matches 5
     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        through
Nucleic
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yu J.;
"Genome sequence of Shigella flexneri 2a: insig through comparison with genomes of Escherichia Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the Buropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentities requires a license agreement (See http://www.isb-sib.ch/ar send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRALN=301 / Serotype 2a;
STRALN=301 / Serotype 2a;
MEDLINE=22272406; PubMedel12384590;
MEDLINE=22272406; PubMedel12384590;
Yang C., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Do
Yang J., Yang F., Zhang X., Zhu J., Kan B., Ding K., Chen
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shigella flexneri.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Pfam, PF00766; ETF alpha; 1.
PROSITE; PS00696; ETF ALPHA; 1.
Electron transport; Flavoprotein;
NP BIND 255
                                                                                                                                          EMBL; AE015041; AAN41705.1; ALT_SEQ. HAMAP; MF 01056; -; 1. PROSITE; PS00696; ETF_ALPHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished observations (APR-2003).

-I- FUNCTION: Required for anaerobic carnitine reduction. May reductant to caiA (By similarity).

-I- PATHWAY: Carnitine metabolism (conversion of Carnitine to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rivoire C.;
Unpublished
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                                                                     Electron transport; Flavoprotein; FAD.

NP_BIND 255 283 FAD (ADP PART) (POT
SEQUENCE 313 AA; 33483 MW; 416CFEC6F0994066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONCEPTUAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBÛNIT: Heterodimer of fixA and fixB (By similarity).
SIMILARITY: BELONGS TO THE ETF ALPHA-SUBUNIT / FIXB FAMILY.
CAUTION: This is a conceptual translation, a stop codon in
position 264 was translated as Gln to maximize the similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          butyrobetaine).
                                                                                                                                                                                                                                                                                                                                                                                                                                      orthologs.
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OR SF0039.
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42
313 AA;
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33513 MW;
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55.6%;
     74.48;
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Last annotation updat
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Pred. No. 19;
2; Mismatches
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ichia coli K12
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                                                                          (POTENTIAL)
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RESULT 9
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PRINTS; PR00336; LYSASSOCTDMP.

PROSITE; PS00311; LAMP_1; 2.

PROSITE; PS00311; LAMP_2; 1.

Transmembrane; Glycoprotein; Lys
SIGNAL 22 407 LY:
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P49129;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Lysosome-associated membrane glycoprotein 1 p
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          CARBOHYD
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Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                               CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                   EMBL; L18986; AAC37682.1; -.
                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane glycoproteins.";
Cell. Mol. Biol. Res. 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uthayakumar S., Granger B.L.; "Cell surface accumulation of overexpressed hamster lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97021428; PubMed=8867788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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FUNCTION: PRESENTS CARROLYDRATE LIGANDS TO SELECTINS.

IMPLICATED IN TUMOR CELL METASTRASIS (BY SIMILARITY).

SUBCELLULAR LOCATION: Type I membrane protein. Lysoson

THIS PROTEIN SHUTTLES BETWEEN LYSOSOMES, ENDOSOMES, AV

MEMBRANE (BY SIMILARITY).

PTM: O- AND N-GLYCOSYLATED; SOME OF THE N-GLYCANS ATTP

LAMP-1 ARE POLYLACTOSAMINOGLYCANS (BY SIMILARITY).

SIMILARITY: BELONGS TO THE LAMP FAMILY.
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BY SIMILARITY.
LYSOSOME-ASSOCIATED
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Sciurognathi; Muridae;
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RESULT 10
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Cederberg H., Hom
Cederberg F.K.;
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P25623; P25622;
01-MAY-1992 (Rel. 22, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 96.1 kDa protein in RIM1-RPS14A intergenic
YCR030C OR YCR30C/YCR29C.
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CARBOHYD
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                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                 Gromadka R.;
Submitted (J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
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                                                                                                                                      Hypothetical SEQUENCE 8
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SIMILARITY: SOME, TO
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75.0%;
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POMBE SPBC4C3.06.
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Pred. No. 26;
0; Mismatches
                                                                   Score 29; DB
Pred. No. 59;
1; Mismatches
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P45469;
01-NOV-1995
16-OCT-2001
16-OCT-2001
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Q935Z2;
28-FEB-2003
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SERAIN=K12 / MG165;
STRAIN=812 / MG165;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A
Blattner F.R., Collado-Vides J., Glasner J.D.,
Riley M., Collado-Vides J., Kirkpatrick H.A.,
REVISIONS TO 196 AND 247.

Holtman C.K., Socias T., Mohler B.J., Chen Y., Youderian P., Sandoval P., Gonzalez A., Salina Submitted (NOV-2002) to the EMBL/GenBank/DDBJ-I- CATALYTIC ACTIVITY: Sn-glycerol 3-phosphate glycerone phosphate + NAD(P)H.
                                                                                                                                                                                                       15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glycerol-3-phosphate dehydrogenase [NAD(P)+]
dependent glycerol-3-phosphate dehydrogenase)
GPSA OR SEA0004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U18997; AAA57955.1; ALT_INIT.
EMBL; AE000396; AAC76186.1; ALT_INIT.
EcoGene; EG12783; yraR.
                                                                                                                                                                              Synechococcus sp. (strain
Bacteria; Cyanobacteria; (
                                                                                                                                                                                                                                                                                                            SYNP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Complete proteome. SEQUENCE 211 AA; 23198 MW; 5E3793BBADC891FF
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YRAR OR B3152
                                                                                         Holtman C.K., Socias T., Youderian P.; 'Synechococcus elongatus Submitted (SEP-2001) to t
                                                                                                                                           SEQUENCE FROM N.
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Science 277:1453-1474(1997).
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HANAD; MF 00394; -; 1.

InterPro; IPR006168; NAD Gly3P dh.

InterPro; IPR006109; NAD Gly3P dom.

Pfam; PF01210; NAD Gly3P dh; 1.

PF01210; NAD Gly3P dh; 1.

PROSITE; PS00957; NAD G3PDH; 1.

Phospholipid blosynthesis; Oxidoredu.

SEQUENCE 308 AA; 32263 MW; 6D952
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between the Swiss I
the European Bioinfo
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Mitochondrial 28S ribosomal protein S30 (S30mt)
cell death protein 9) (BM047).
MRPS30 OR PDCD9.
                                                                                        WEDLINE-21154917; PubMed=11230166; Wightine-21154917; PubMed=11230166; Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl Miemann S., Weil B., Wellenreuther H., Bauersachs S., Blum H., Ansorge W., Boecher M., Bloecker H., Koehrer K., Strack N., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner Wambutt R., Korn B., Klein M., Poustka A.; Tampe J., Heubner "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."; Genome Res. 11:422-435(2001).
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MEDITUS=20108792, PubMed=10640817;
Carim L. Sumoy L. Nadal M. Esti
"Cloning, expression, and mapping,
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Submitted
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[2]
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TISSUE=Teratocarcinoma;
Isogai T., Ota T., Nish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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MW; 6D9526DF5A8C8A77 CRC64;
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RX MEDIING=2038257, PubMed=12477932;

RX MEDIING=22388257, PubMed=12477932;

RA MISCHUNG=22388257, PubMed=12477932;

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Shat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Shat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Shat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Robristein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McZwan P.C., McKernan K.J., Malek J.A., Gay L.J., Hulky S.W.,

RA Pahey J., Helton E., Kettenan M., Madan A., Rodrigues S., Sanchez A.,

RA Pahey J., Helton E., Kettenan M., Madan A., Rodrigues S., Sanchez A.,

RA Pahey J., Helton E., Kettenan M., Madan A., Rodrigues S., Sanchez A.,

RA RA RAHISCHUM M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA RA RAHISCHUM M., Madan A., Schautz J., Myers R.M.,

RA RAGRIGUEZ A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.",

RY Maran M., Schein J.E., Jones S.J.M., Maran M.A.,

RY Perc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Word E.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.;

"The small subunit of the mammalian mitochondrial ribosome: identification of the full complement of ribosomal proteins prese.

J. Biol. Chem. 276:19363-19374 (2001).

SUBUNIT: Component of the mitochondrial ribosome small subuni (288) which comprises a 125 rRNA and about 30 distinct protein.

SUBCELLULAR LOCATION: Mitochondrial.

TISSUE SPECIFICITY: Heart, skeletal muscle, kidney and liver. Lower expression in placenta and peripheral blood leukocytes.

CAUTION: Ref. 6 sequence differs from that shown due to a numb sequencing errors that include frameshifts.
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EMBL; AL355715; CAB90810.1; -...
EMBL; AL355716; CAB90811.1; -...
EMBL; AL35706; CAB60811.1; -...
EMBL; AK074777; BAC11202.1; -...
EMBL; BC007735; AAH07735.1; -...
EMBL; BC007735; AAH07735.1; ALT_FRAME.
Genew; HGN0:8795; MRPS30.
GO; GO:0006915; P:apoptosis; TAS.
Ribosomal protein; Mitochondrion.
CONFLICT 82 82 82 8 -> C (IN SEQUENCE 439 AA; 50348 MW; ADD564743 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch). S -> C (IN REF. 4 / I -> V (IN REF. 3). ; AD0564743E03290C . Usage by and for http://www.isb-sib. AND CRC64; restrictions and for ņ g

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Query Match Best Local

71.8%; 75.0%;

Score 28; DB Pred. No. 49;

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Length 439;

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RESULT 14

RT30 MM
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RA Arzkawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubhi F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Schriml L.M., Staubhi F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninoi P., de Bonaldo M.P.,
RA Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Ming B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Havashizaki Y...
                                                                                                                 X MEDLINE-TUNN, TISSUE-Breast;
XX MEDLINE-Z388257; PubMed=12477932;
X MEDLINE-Z388257; PubMed=12477932;
X MEDLINE-Z388257; PubMed=12477932;
X MEDLINE-Z388257; PubMed=12477932;
X MILLINE-Z388257; PubMed=12477932;
X Maltschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
X Maltschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
X Matchins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
X Matchins R.F., Jordan H., Moore T., Max S.I., Rubin G.M., Hong L.,
X Matchins R.F., Jordan H., Moore T., Rasavant T.L., Scheetz T.E.,
X Matchins R.F., Jordan N.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
X Matchins R.F., Jordan N.B., Peters G.J., Abramson R.D., Mullahy S.J.,
X Stapleton M., Soders G.J., Abramson R.D., Mullahy S.J.,
X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
X Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
X Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
X Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
X Matching M., Madan A., Young A.C., Shevchenko Y., Bouffeard G.G.,
X Miting M., Madan A., Young A.C., Shevchenko Y., Bouffeard G.G.,
X Miting M., Madan A., C., Scheutz J., Myers R.M.,
X Matchins M., Madan A., Schein J.E., Jones S.J.M., Warra M.A.,
X Matchins M., Madan A., Schein J.E., Jones S.J.M., Warra M.A.,
X Generation and initial analysis of more than 15,000 full-length
N Matchins M. M. Matchins M. J., Salaka U., Smailus D.E.,
X Matchins M. M. Matchins M. J., Salaka U., Smailus D.E.,
X Matchins M. M. M., Schein J.S., Matchins M. J., Salaka U., Smailus D.E.,
X Matchins M. M. M., Schein J. W., Matchins M. J., Salaka U., Smailus D.E.,
X Matchins M. M. M., Matchins M. J., Salaka U., Smailus D.E.,
X Matchins M. M. M., Matchins 
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Q9D0G0; Q9CYS8; Q9JJQ2;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Mitochondrial 28S ribosomal protein S30 (S30mt) (MRP-S30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                SEQUENCE OF
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Best Local
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=S288C;
STRAIN=S288C;
MEDLINE=96437976; PubMed=8840504;
Huang M.-E., Manus V., Chuat J.-C., Galibert F.;
"Analysis of a 62 kb DNA sequence of chromosome"
"ain" frames and a gene cluster with a counter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YJ48 YEAST
P47125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosomal
CONFLICT
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                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 50.8 kDa protein in MIR1-STE18 i.
YJR078W OR J1840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AX011476; BAB27644.1; --
EMBL; AX013360; BAB28809.1; ALT FRAME.
EMBL; BC029784; AAH229784.1; --
EMBL; BL355710; CAB90812.1; --
EMBL; AL355710; CAB90812.1; --
EMBC; MGI; 1926237; Mrps30.
                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEAST
                                    EMBL; Z49578; CAA89606.1; EMBL; L47993; AAB39303.1;
                                                                                                                                                                                   Yeast 12:869-875(1996).
-!- SIMILARITY: BELONGS TO THE INDOLEAMINE 2,3-DIOXYGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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127
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P -> SPS (IN REF. 2).
RPR -> QPG (IN REF. 2).
H -> N (IN REF. 1; BAB2880;
W; C35A540D3A524BCC CRC64;
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Pred. No. 49;
1; Mismatches
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PIR; S57097; S57097. SGD; S0003839; YJR078W. GO; GO:0005737; C:cytop

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DR GO; GO:0009435; P:nicotinamide adenine dinucleotide biosynthesis; IMP.

DR pfam; pF01231; IDO; 1.

DR pROSITE; p800876; IDO 1; 1.

DR PROSITE; p800877, IDO 2; 1.

ET METAL 375 375 IRON (HEME PROXIMAL LIGAND) (POTENTIAL).

FT METAL 375 375 IRON (HEME PROXIMAL LIGAND) (POTENTIAL).

SQ SEQUENCE 453 AA; 50775 MW; A8BF1702F6827EC9 CRC64;

Query Match 71.8%; Score 28; DB 1; Length 453;

Best Local Similarity 75.0%; Pred. No. 51;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 284 GSNAQSSL 291

Search completed: January 29, 2004, 14:53:08

Job time: 6.82353 secs
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Result
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Perfect score:
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Maximum DB
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1: sp_archea:*
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5: sp_invertebrat:
6: sp_mammal:*
7: sp_mhc:*
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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Listing first 45 summaries
   sp_invertebrate:*
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Q922t9 mus musculu
Q8vh34 mus musculu
Q9dc13 mus musculu
Q33586 staphylococ
Q8w459 arabidopsis
Q9pn15 campylobact
Q55632 synechocyst
Q81552 hepatitis c
Q81897 arabidopsis
Q8wqa0 caenorhabdi
Q8s2e4 oryza sativ
Q23998 hordeum vul
Q89281 oryza sativ
Q99410 pseudomonas
Q8p956 xanthomonas
Q8p956 xanthomonas
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17 30 76.9 118 30 76.9 119 30 76.9 20 30 76.9 21 30 76.9 22 30 76.9 23 30 76.9	250 333 334 425 686 737		Q9ZUA5 Q34933 Q9XEN7 Q8RGQ9 Q8TBB6 Q8TBB6 Q8BXR1
5 30 76. 6 30 76. 7 29 74.	95 70	0 0	Q94C93 Q9VF35 Q8XWF4
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0 29 74. 1 29 74.	14	16 17	Q8Y328 O8TLI9
2 29 74.	42	16	08X3U
3 29 74. 4 29 74.	8 6	ທ ທ	Q81812 09NAL0
5 29 74.	30	16	Q986D7
6 29 74. 70 74	л U	16	Q8X2R1
8 29 74.	72	ហ	Q95XI5
9 29 74.	76	10	Q9SHG5
0 29 74. 1 29 74.	888	10	Q9FFE8
2 29 74.	95	16	Q8PPS2
3 29 74.	86	16	Q8P527
4 29 74.	4	10	00,000
5 29 74.	អ		107470

ALIGNMENTS

Q922T9 PRELIMINARY; PRT; 189 AA.
Q922T9;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to lysosomal membrane glycoprotein 1 (Fragment).
Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI TaxID=10090;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

SEQUENCE FROM N.A.

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RESULT
Q8VH34
ID Q8
AC Q8
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Best Local S
Matches
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006785; AAH06785.1; -
InterPro; IPR002000; Lamp.
Pfam; PF01299; Lamp; 1.
PRINTS; PR00336; LYSASSOCTDMP.
PROSITE; P800310; LAMP_1; 1.
PROSITE; P800311; LAMP_2; 1.
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NO
Q8VH34 PRELIMINARY;
Q8VH34;
Q1-MAR-2002 (TrEMBLrel. 20,
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             Created)
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Pred. No.
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P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

A Cho K., Han J.;

KL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AY069968; AAL58070.1; -.

DR InterPro; IPRO02000; Lamp;

DR Pfam; PF01299; Lamp; 1.

DR PRINTS; PR00316; LYSASSOCTEMP.

DR PROSTTE; PS00310; LAMP 1; 2.

DR PROSITE; PS00311; LAMP 1; 2.

DR PROSITE; PS00311; LAMP 2; 1.

OF PROSITE; PS00311; LAMP 2; 1.
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Matches
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XX MEDIXINE_21085660; PubMed=11217851;
XX MEDIXINE_21085660; PubMed=11217851;
XX MEDIXINE_21085660; PubMed=11217851;
XX MEDIXINE_21085660; PubMed=11217851;
XX MARIAN J., Shibata X., Yoshino M., Itoh M., Ishii Y.,
XX Araka X., Izawa M., Nishi X., Kiyosawa H., Kondo S., Yamanaka I.,
XX Alzawa K., Izawa M., Nishi X., Kiyosawa H., Kondo S., Yamanaka I.,
XX Alzawa K., Izawa M., Nishi X., Kyosawa H., Kando S., Casavant T.,
XX Araka Y., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
XX Araka Y., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
XX Araka M., Matsuda T., Misaido I., Pasole G., Quackenbush J.,
XX Araka M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,
XX Araka Y., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
XX Araka Y., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
XX Araka Y., Barsh G.,
XX Araka Y., Barsh G.,
XX Araka Y., Matsuda Y., Manja N., Carninci P., de Bonaldo M.F.,
XX Araka Y., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
XX Araka Y., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
XX Araka Y., Storch K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
XX Araka Y., Yoshida K., Hasegawa Y., Xawaji H., Kohtsuki S.,
XX Araka Y., Yoshida K., Hasegawa Y., Xawaji H., Kohtsuki S.,
XX Araka Y., Yoshida K., Hasegawa Y., Xawaji H., Kohtsuki S.,
XX Araka Y., Yoshida K., Hasegawa Y., Xawaji H., Kohtsuki S.,
XX Araka Y., Yoshida K., Hasegawa Y., Xawaji H., Kohtsuki S.,
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Lysosomal membrane glycoprotein 1.
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Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                             Wynshaw-Boris A., Yoshida K.
Hayashizaki Y.,
"Functional annotation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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PROSITE; PS00310; LAMP_1;
PROSITE; PS00311; LAMP_2;
SEQUENCE 407 AA; 43936
                                                                                   InterPro; IPR002000; Lamp. Pfam; PF01299; Lamp; 1. PRINTS; PR00336; LYSASSOCTDMP
                                                                                                                                                                             EMBL; AK004637; BAB23428.1; MGD; MGI:96745; Lampl.
                                                                                                                                                                                                                                Nature 409:685-690(2001)
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Rodentia;
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77.8%;
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Pred. No.
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Sciurognathi; Muridae;
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Sciurognathi; Muridae; Murinae; Mus.
   696D0C79F627DA84 CRC64;
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annotation update)
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Best Local
Q8W455;
Q8W455;
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 10.2 kDa protein (Fragment).
Arabidopsis thaliana (Mouse-ear oress).
Arabidopsis thaliana (Mouse-ear oress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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O33586, O1-JAN-1998 (TREMBLrel. 05,
01-JAN-1998 (TREMBLrel. 05,
01-MAR-2002 (TREMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SPECIES-S.aureus; STRAIN-SA502A;

MEDLINE-97342847; PubMed-9197262;

Ji G., Beavis R., Novick R.P.;

"Bacterial interference caused by autoinducing Science 276:2027-2030(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGRD OR SAV2037 OR SA1842.1 OR SAS066.
Staphylococcus aureus (strain Mu50 / ATC
Staphylococcus aureus (strain N315), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lancet 357:1225-1240(2001).

EMBL; AP003136; BAB58196 1; -.

EMBL; AP003364; BAB58199 1; -.

EMBL; AP003135; BAB43124.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
Muroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayash
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito
Seximizu K., Hirakawa H., Xuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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AGRD OR SAV2037 OR SA1842.1
                                                                                                                                                                                                                                                                                Q8W459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "whole genome sequencing of meticillin-resistant Staphylococcus
aureus.";
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77.8%;
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I., Kaito C.,
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Nature 403:665-668(2000)
EMBL; AL139077; CAB73354 1; -.
Interpro; IPR004438; PepF
Interpro; IPR001567; Peptidase M3.
Interpro; IPR006025; Zn_MTpeptdse.
Pfam; PF01432; Peptidase M3; 1.
TIGRFAMS; TIGR00181; pepF; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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Q9PNJ5;
01-OCT-2000
01-OCT-2000
01-MAR-2003
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SEQUENCE FROM N.
Q55632
Q55632;
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                           STRAIN=NCTC 11168;
MEDLINE=20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd
Jagels K., Karlyshev A., Woule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                   Campylobacter jejuni.
Bacteria; Epsilonproteobacteria;
Campylobacteraceae; Campylobacter.
CMBI_TaxID=197;
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SEQUENCE
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Q1-NOV-1996;
Q1-NOV-1996;
Q1-OCT-2002
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MEDLINB=97061201; PubMed=8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Miyajima N., Hirosawa M., Sugiura M., Makazaki N., Naruo K., Okumu
Hosouchi T., Matsuno A., Muraki A., Wakazaki N., Naruo K., Okumu
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda
Tabata S.;
   SEQUENCE FROM N.A.
STRAIN=NE145;
MEDLINE=94201770; Pul
Tokita H., Shrestha (
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EMBL; D64000; BAA10146.1; -.
InterPro; IPR002549; UPF0118.
Pfam; PF01594; UPF0118; 1.
Pfam; PF01594; UPF0118; 1.
Hypothetical protein; Complete SEQUENCE 340 AA; 37941 MW;
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Kaneko T., Tanaka A., Sato
Sugiura M., Tabata S.;
"Sequence analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=PCC 6803;
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Bacteria; Cyanobacteria;
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SLR0784.
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Hypothetical protein slr0784
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                                                                                                                                        MEDLINE=94186155; PubMed=8138250;
Shrestha S.M., Tsuda F., Okamoto H., Tokita H., Hc
Tanaka T., Miyakawa Y., Mayumi M.;
"Hepatitis B virus subtypes and hepatitis C virus
patients with chronic liver disease in Nepal.";
Hepatology 19:805-809(1994).
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A., Sato S., Kotani
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
nara-xvian endohydrolase -like protein (Beta-xylan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; Rosidae;
eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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                                    EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL031394; CAR20594.1;

EMBL; AL161584; CAB80098.1;

EMBL; AL161580; CAB80098.1;

InterPro; IPR001000; Glyco_hydro_10.
InterPro; IPR001000; Glyco_hydro_10;
SMART; SM00633; Glyco_hydro_10; 1.
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Heijnen L., Vos P., Mewes H
Submitted (AUG-1998) to the
                                                                                                                                                                                                         SEQUENCE OF 1-0 FROM N.A. VITALE D., Liguori R., Argiriou Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBI
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Obermaier B., Deutschenbaur
Mayer K.F.X.;
Submitted (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
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  Hydrolase.
SEQUENCE
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Q8WQA0;
Q1-MAR-2002 (TYEMBLY
01-MAR-2002 (TYEMBLY
01-MAR-2003 (TYEMBLY
Y105E8A.24 protein.
  STRAIN-CV. Nipponbare;
Sasaki T., Mateumoto T., Y
"Orya sativa nipponbare(G
clone:P0022P10.")
Submitted (FEB-001) to th
.i- SIMILARITY: BELONGS TG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          investigating biology .; section 282:2012-2018 (1998). Science 283:2012-2018 (1998). EMBL, AL132876; CAD21673.1; -WOXMPap; Y105E8A.24; CE29942.
                                                                                                                                                                                                                                                                                                                                            Q8S2E4
Q8S2E4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                      Oryza sativa (japonica cultivar-group).
Bukaryota, Viriddiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pos
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                Putative P-glycoprotein. P0022F10.15.
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                                                                                                                   SEQUENCE FROM N.A.
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    the EMBL/GenBank/DDBJ databases TO THE ABC TRANSPORTER FAMILY.
                                                           Yamamoto
(GA3) geno
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Pred. No. 1.2e+02;
1; Mismatches 2;
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Pred. No. 2.6e+02;
2; Mismatches 1
                                                         genomic
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InterPro; IPR001140; ABC_TM_transpt.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
ProDom; PD000006; ABC_transporter; 2.
ProDom; PD000006; ABC_transporter; 2.
SMART; SM00382; AAA; 7.
PR05TTE; PS00211; ABC_TRANSPORTER; 2.
ATP-binding; Transport.
ATP-binding; Transport.
SEQUENCE 1203 AA; 131507 MW; B78383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003593; AAA ATPASE.
InterPro; IPR001140; ABC TM_transpt.
InterPro; IPR003439; ABC transporter.
Pfam; PF000664; ABC membrane; 2.
Pfam; PF00005; ABC transporter; 2.
ProDom; PD000005; ABC transporter; 2.
SMART; SM00382; AAA; 2.
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                 01-MAR-2003
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01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                      Q8GU81;
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Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=cv. Maris Mink;
MEDLINE=98019088; PubMed=9358056;
Davies T.G.E., Theodoulou F.L., Hallahan
Davies T.G.E., Theodoulou F.L., Hallahan
"Cloning and characterization of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          023998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4513;
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Last sequence up
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2; Mismatches
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2.7e+02;
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a; Poales; Poaceae; Pooideae;
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1es 1;
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RESULT 15
Q8PQ96
ID Q8PQ9
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SEQUENCE FROM N.A.

SETARINATCO 15692 / DAO1;

SCOURT C.K., Phan X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA Stover C.K., Phan X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Warner C.-Washin S., Yuan Y.,

RA Bardy L.L., Collter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

RC "Complete genome sequence of Pseudomonas aeruginosa PAO1, an

Opportunistic pathogen.";

RT Opportunistic pathogen.";

REMBL, ABO04918; ABG07404.1;

DR Hypothetical protein; Complete proteome.

SQ SEQUENCE 213 AA; 23164 MW; ADBAFF71FB56306F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 6
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Best Local &
Matches
                                                                       Q8PQ96;
Q8PQ96;
01-0CT-2002
01-0CT-2002
01-0CT-2002
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9HX10;
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EMBL, AJ53055; CAD59577.1; -.
SEQUENCE 1234 AA; 134571 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gamm
Pseudomonadaceae; Pseudomonas.
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Tasinski M., Ducos E., Martinoia E., Boutry M.,

"The ATP-binding cassette transporters: structure,

"The ATP-binding cassette transporters: structure,
                        Hypothetical XAC0432.
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Similarity 66.7%;
6; Conservative
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(TrEMBLrel. 16, 1
. (TrEMBLrel. 18, 1
l protein PA4017.
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axonopodis
                                                                       (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                   PRELIMINARY;
                                                 protein XAC0432.
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66.7%;
(pv. citri).
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 74;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30; DB Pred. No. 74;
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RC STRAIN=306 / ATCC 11902 / XV 101;

RC STRAIN=306 / ATCC 11902 / XV 101;

RX MEDLINE=22022145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Camargo L.E.A.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Ciarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Spinola J.C., Kitajima J.P.,

RT Tindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.,

RA Gruber A. AEO11670, AAM35323.1;

RM Mature 417:459-463(2002).

RE MBL, AEO11670, AAM35323.1;

Complete proteome.

SEQUENCE 226 AA, 24311 MW, 1CD4F9E1F4E39DAC CRC64;
Search completed: January 29, 2004, 14:56:45 Job time : 28.8676 secs
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66.78;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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        protein search, using sw model
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length: 2000000000
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Match
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1: /cgn2_6/ptodatta/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodatta/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/FTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
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39
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      GANAXSSLF
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Copyright (c) 1993 - 2004 Compugen Ltd.
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      BB
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                              US-09-339-511-2
US-08-861-476C-6
US-08-861-476C-6
US-08-861-476C-6
US-09-39-511-6
US-09-39-511-6
US-09-339-511-6
US-09-556-916-32
US-09-556-916-32
US-09-556-916-32
US-09-556-916-28
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US-09-558-916-28
US-09-558-916-28
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US-09-339-511-7
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Sequence 2, Appli
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Sequence 6, Appli
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Sequence 30, Appli
Sequence 21, Appli
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Sequence 16, Appli
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US-09-339-511-1
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US-09-339-511-2
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SEQ ID NO 2
LENGTH: 9
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Result No.

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08-08-09-561-2 09-311-807A-2 09-311-7807A-2 09-311-7807A-2 09-311-7807-211-2 09-557-211-2 00-488-1138-5 08-488-1138-5 08-488-1138-5 08-488-1138-5 09-136-389-57 09-136-389-57 09-136-389-57 09-136-389-57 09-136-389-57 09-136-389-57 09-136-389-57 09-136-389-57 09-136-389-57 09-136-389-57 09-136-389-57 09-136-389-57 09-136-389-57 09-162-843A-3 09-869-933-328

ALIGNMENTS

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APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Patricia
APPLICANT: No. 6337395ick, Richard P.
APPLICANT: No. 6337395ick, Richard P.
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
ITILE OF INVENTION: INTERFERENCE
FILLE OF INVENTION: INTERFERENCE
FILLE REPERENCE: 600-1-231N
CURRENT APPLICATION UNMER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 600/990,402
PRIOR APPLICATION NUMBER: 600/990,402
PRIOR APPLICATION NUMBER: 600/990,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                     ; Sequence 1, Application ; Patent No. 6337385 ; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
Muir, Tom
Mayville, Patricia
No. 6337385ick, Richard F
Beavis, Ronald
Ji, Guangyong
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100.0%; Pred. No.
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Best Local Similarity
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US-08-861-476C-3
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Patent No. 6447786
                                                   SOFTWARE: PatentIn version 3.0 SEQ ID NO 6
                                                                                                                                                                                                                Sequence 6, Application US/08861476C Patent No. 6447786
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Best Local
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                                                                                        CURRENT APPLICATION NUMBER: US/08/861,476C CURRENT FILING DATE: 1997-05-22 NUMBER OF SEQ ID NOS: 8
                                                                                                                    INFORMATION:

APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE: 63753/7
                                                                                                                                                                                                                                                    -08-861-476C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/861,476C CURRENT FILING DATE: 1997-05-22 NUMBER OF SEQ ID NOS: 8
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CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE: 63753/7
ORGANISM: Staphylococcus aureus
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COTHER INFORMATION: Xaa represents any amino acid at this position.
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77.8%;
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Pred. No.
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Pred. No.
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                                                                                                                                                  NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
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Best Local
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Best Local :
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                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
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CURRENT APPLICATION NUMBER: US/09/595,857B
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 60/141,543
PRIOR FILING DATE: 1999-06-28
                                                                                                                                                                                                                                                                   APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
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APPLICANT: Chen, Nancy J.
TITLE OF INVENTION: PLANT XYLANASES
                                          FEATURE:
OTHER INFORMATION: Description
OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Arabidopsis thaliana
                  NAME/KEY: VARIANT LOCATION: (5)
                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Xaa represents any amino acid at this position
                                                                                                                                 ENGTH:
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NO. 6495743
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Similarity 66.7%;
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Mayville, Patricia
No. 6337385ick, Ri
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Pred. No.
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Pred. No.
                                                                 of Artificial Sequence: Synthetic
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Query Match

76.98;

Score 30;

DB 4;

Length

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US-09-328-352-7790
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                                                                                                                        ; ORGANISM: Acinetobacter baumannii
US-09-328-352-7790
                                                                                                                                                                                                                                           GENERAL INFORMATION: Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: EAUMAINII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7790
                                                            Matches
                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                          Sequence
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Best Local
                                                                                                                                                                                                                                                                                                                           Sequence 7790, App
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: I OTHER INFORMATION: I NAME/KEY: VARIANT LOCATION: (5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
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PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                       LENGTH: 222
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa represents any amino acid
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120 GANANSPIF 128
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                                                          Similarity 66. 6; Conservative
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7; Conservative
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6337385
                            GANAXSSLF 9
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No. 6337385ick, Richard
Beavis, Ronald
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BER: 60/090,402
                                                                         76.9%;
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77.8%;
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                                                        Score 30; DB . Pred. No. 28; 1; Mismatches
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Pred. No. 2.5e
1; Mismatches
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1; Mismatches 1
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2.5e+05;
                                                                                          DB 4;
                                                                                        Length 222;
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                                                                                                       US-09-252-991A-21944
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US-09-556-916-30
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CURRENT FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
                                                       Sequence 21944, Appl Patent No. 6551795
GENERAL INFORMATION:
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SEQ ID NO 32
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Best Local :
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                                             APPLICANT:
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CURRENT FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Friedrich, Glenn
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TYPE: PRT
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APPLICANT: Sands, Arti
FILE REFERENCE:
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APPLICANT: Nehls, Michael
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          PPLICANT: Marc J. Rubenfield et al.
ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
ITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT: Sands, Arthur T.
ITLE OF INVENTION: No. 6548271el Human Transporter Proteins
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                                                                                                                                                                   150 GASALSSMF 158
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NT: Turner, Alex
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6; Conserve
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                                                                                      Application US/09252991A
107196.136
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Pred. No. 33;
2; Mismatches
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             SEQUENCES RELATING TO AND THERAPEUTICS
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CURRENT APPLICATION NUMBER: US/09/556,916
CURRENT FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 28
LENGTH: 672
TYPE: BRI
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                          Sequence 28, App
Patent No. 6548
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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LENGTH: 672
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APPLICANT: Turner, Alex
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LENGTH: 298
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-09-556-916-26
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEC ID NOS: 33142
                                                                                                                             APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6548271el Human Transporter Proteins
FILE REFERENCE: 8535-041-999
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ITLE OF INVENTION: No. 6548271el Human Transporter Proteins
ILE REFERENCE: 8535-041-999
URRENT APPLICATION NUMBER: US/09/556,916
URRENT EILING DATE: 2000-04-21
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NT: Turner, Alex
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                                                                   FastSEQ for Windows Version 3.0
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Friedrich, Gle
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Friedrich, Gle
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548271
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66.7%;
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Pred. No.
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Pred. No.
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; Sequence 7, Application US/09339511
; Patent No. 6337385
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Matches 6
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Best Local S
Matches 6
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LENGTH: 1380
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SEQ ID NO 7
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APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                   APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: No. 6337385ick, Richard
                                                 OTHER INFORMATION:
OTHER INFORMATION:
NAME/KEY: VARIANT
                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                             FEATURE:
OCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position.
                                                                                                                                                                 ENGTH:
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                                                                   Description of peptide
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Pred. No. 3.
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Pred. No.
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                                                                                           Artificial Sequence: Synthetic
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		Db 1 GVNAXSAF 9 Search completed: January 29, 2004, 15:03:20 Job time : 11.1176 secs	Query Match 71.8%; Score 28; DB 4; Length 9; Best Local Similarity 77.8%; Pred. No. 2.5e+05; Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps Qy 1 GANAXSSIF 9
			0;

Sequence 2, Appli Sequence 37, Appli Sequence 37, Appl Sequence 3629, A Sequence 3629, Appl Sequence 1194, Ap Sequence 118, Appl Sequence 18, Appl Sequence 18, Appl Sequence 356, Appl Sequence 356, Appl Sequence 2765, Ap Sequence 6581, Ap Sequence 6581, Ap Sequence 6239, Ap Sequence 6239, Ap Sequence 4301, Ap Sequence 2791, Appl Sequence 2791, Appl Sequence 14307, Ap Sequence 56, Appl Sequence 56, Appl Sequence 1547, Appl Sequence 279, Appl Sequence 279, Appl Sequence 279, Appl

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                         Score
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

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     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-10-201-444-6
US-10-201-444-6
US-10-32-950-6
US-10-368-687-30
US-10-368-687-32
US-10-368-687-28
US-10-368-687-28
US-10-1368-687-28
US-10-1368-687-28
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73.223 Million cell updates/sec
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Publication No. US20020077453A1

GENERAL INFORMATION:

APPLICANT: Muir. Tom
APPLICANT: Mo. US20020077453A1ick, Richard P.
APPLICANT: No. US2002000077453A1ick, Richard P.
APPLICANT: No. US20020077453A1ick, Richard P.
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                                                                         Query Match
Best Local S
Matches
                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Ar
OTHER INFORMATION: peptide
NAME/KEY: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents an
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100.0%; Pred. No. 7e+05;
tive 0; Mismatches 0; Indels
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13 US-10-108-260A-4061
12 US-10-108-260A-4061
12 US-10-407-079-37
12 US-10-407-079-37
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14 US-10-291-265-78
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18 US-10-388-6781-444
28 US-10-388-6781-4547
18 US-09-864-291-279
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US-10-201-444-3
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                                                                 Query Match
Best Local S
Matches
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CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PAtentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                      PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
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Publication No. US20030078378A1
GENERAL INFORMATION:
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Best Local :
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APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453Alick, Richard
                                                                                                                                                                                                                                                                         APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIF
FILE REFERENCE: 63753/7
CURRENT APPLICATION NUMBER: US/10/201,444
CURRENT FILING DATE: 2002-07-23
CURRENT FILING DATE: US/08/861,476
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TITLE OF INVENTION: NOTER FERENCE
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
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COTHER INFORMATION: Xaa represents any amino acid at this position.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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mes 8; Conserv
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                                                               h 82.1%;
Similarity 77.8%;
7; Conservative
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Pred. No.
                                                                 Score 32; DB 15;
Pred. No. 7e+05;
0; Mismatches 2
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RESULT 4 US-10-201-444-6

> RESULT 6 US-10-032-950-6

Sequence 6, Application US/10032950 Publication No. US20020077453A1 GENERAL INFORMATION:

APPLICANT: Muir,

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Sequence 6, Application US/10201444
Publication No. US20030078378A1
GENERAL INFORMATION:
APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRUL
FILE REFERENCE: 63753/7
CURRENT APPLICATION NUMBER: US/10/201,444
CURRENT FILING DATE: 2002-07-23
PRIOR FILING DATE: 1997-05-2
PRIOR FILING DATE: 1997-05-2
NUMBER OF SEQ ID NOS: 8
COPTMAND: Dates of SEQ ID NOS: 8
                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequ
OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid
US-10-032-950-5
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 9
                                                                                          Query Match
Best Local
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APPLICANT: Mayville, Patricia
APPLICANT: Mo. US20020077453Alick, Richard
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
                                                                        Matches
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TITLE OF INVENTION: INVEL STAPHYLOCOCCUS PEPTIDES
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILLING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 66/090,402
PRIOR APPLICATION NUMBER: 66/090,402
PRIOR FILING DATE: 1998-66-24
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
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                                  1 GANAXSSLF 9
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77.8%;
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Pred. No. 5.1;
                                                                                          Score 30; DB 13
Pred. No. 7e+05;
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RESULT 7
US-10-368-687-30
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                                                                                                                               В
                                                                                                                                                                                                                                                                            ; TYPE: PRT; ORGANISM: Homo sapiens US-10-368-687-30
                                                      RESULT 8
US-10-368-687-32
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LENGTH: 9
TYPE: PRT
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/368,687
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: US/09/556,916
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 258
LENGTH: 258
                                                                                                                                                                                                     Query Match
Best Local S
Matches 6
Sequence 32, Application US/10368687 Publication No. US20030162713A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30, Application US/10368687
Publication No. US20030162713A1
GENERAL INFORMATION:
APPLICANT: Turner, Alex
APPLICANT: Zambrowicz, Brian
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Best Local
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CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nehls, Michael
APPLICANT: Friedrich, Glenn
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NO. US20030162713A1el Human
FILE REFERENCE: 8535-041-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
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TITLE OF INVENTION: INTERFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                            r MATCH 76.9%;
Local Similarity 66.7%;
les 6; Conservative
                                                                                                                               150 GASALSSMF 158
                                                                                                                                                                  1 GANAXSSLF 9
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No. US20020077453Alick, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beavis,
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77.8%;
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Pred. No. 88;
2; Mismatches
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Pred. No. 7e+05;
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APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Nehls, Michael
APPLICANT: Friedrich, Glenn
APPLICANT: Sands, Arthur T:
ITILE OF INVENTION: No. US20030162713A1el Human Transporter Proteins
FILE REFERENCE: 8535-041-99
CURRENT APPLICATION UNMBER: US/10/368,687
CURRENT FILING DATE: 2003-02-14
PRICR APPLICATION NUMBER: US/9/556,916
PRICR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Turner, Alex
APPLICANT: Turner, Alex
APPLICANT: Turner, Alex
APPLICANT: Nehls, Michael
APPLICANT: Nehls, Michael
APPLICANT: Friedrich, Glenn
APPLICANT: Sands, Arthur T.
ITILE OF INVENTION: NO. US20030162713A1el Human Tre
FILE REFERENCE: 8535-041-999
CURRENT APPLICATION NUMBER: US/10/368,687
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: US/09/556,916
PRIOR APPLICATION NUMBER: US/09/556,916
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEG ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LENGTH: 672
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-368-687-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-368-687-26
; Sequence 26, Application US/10368687
; Publication No. US20030162713A1
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                                                                                                                                                                               GENERAL INFORMATION:
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Best Local Similarity
Matches 6; Conserv
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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APPLICANT: Turner, Alex
APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Friedrich, Glenn
APPLICANT: Sands, Archur T.
TITLE OF INVENTION: No. U820030162713A1el Human Transporter Proteins
FILE REFERENCE: 8335-041-999
CURRENT APPLICATION NUMBER: US/10/368,687
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Local Similarity 66.7%;
es 6; Conservaring
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66.7%;
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Pred. No. 2.5e+02;
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Pred. No. 88;
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US-10-108-605-303
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                 CURRENT APPLICATION NUMBER: US/09/864,408A CURRENT FILLING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: 60/206,690 PRIOR FILING DATE: 2000-05-24 NUMBER OF SEQ ID NOS: 9068 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7538 LENGTH: 122
                                                                                                                                                                                Sequence 7538, Application US/09864408A
Publication No. US20040009474A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shinkets, Richard A.
PITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 303
LENGTH: 1569
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PRIOR APPLICATION NUMBER: US/09/556,916
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 28
LENGTH: 672
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Best Local
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Publication No. US20020160934A1
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                                                                                                                                                                                                                                                                                                                                   -09-864-408A-7538
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PRIOR FILING DAYE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DAYE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
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nes 6; Conserv
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6; Conservative
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66.7%;
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Pred. No. 2.
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Pred. No. 6.1e+02;
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2.5e+02;
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APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUNO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR PILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SEQ ID NO 2461
LENGTH: 491
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US-10-083-357-1280
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IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NACHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
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OTSUKI, TETSUJI
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ISONO, YUUKO
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TAKAO

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Sequence 1280, Application US/10083357

Publication No. US20030054370A1

GENERAL INFORMATION:
APPLICANT: Qiandong Zeng et al.
TITLE OF INVENTION: Systemic Discovery of New Ger
FILE REFERENCE: 032796-090

CURRENT APPLICATION NUMBER: US/10/083,357

CURRENT FILING DATE: 2002-02-27

NUMBER OF SEQ ID NOS: 1346

SEQ ID NO 1280

LENGTH: 255
                                                                                                                         ; TYPE: PRT ; ORGANISM: Saccharomyces cerevisiae US-10-083-357-1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-09-864-408A-7538
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity '/ɔ.u
Conservative
                                                           Best Local Similarity
Matches 6; Conserv
140 GANATSAL 147
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                                1 GANAXSSL 8
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.4%;
                                                                             74.4%;
75.0%;
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; Pred. No. 66;
1; Mismatches
                                                            1; Mismatches
                                                                             Score 29; DB 15;
Pred. No. 1.5e+02;
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                                                                                            Length 255
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US-10-156-761-11286

US-10-156-761-11286, Application US/10156761

Fedurace 11286, Application US/10156761

Fublication No. US20030119018A1

GENERAL INFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11286

LENGTH: 550
TYPE: PRT
ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2461
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Search completed: January 29, 2004, 15:01:45 Job time : 26.5441 secs
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                                                                                                                                                                              Query Match 74.4%; Score 29; DB 15; Length 550; Best Local Similarity 66.7%; Pred. No. 3.3e+02; Matches 6; Conservative 0; Mismatches 3; Indels
                                                                                             470 GANESSDLF 478
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|||: |::|
2 GANSTSAVF 10
                                                                                                                                       1 GANAXSSLF 9
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Çəs
           protein search, using sw model
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length: 2000000000
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Match
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.nnm...
3: /SIDS1/gcgdata/nannnn--/
                                                                                                                                                                                                                                                                                                                                                                                                                                               22221111111111
32109875543210:
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Gapop 10.0 , Gapext 0.5
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37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1107863 segs, 158726573 residues
         94.66
94.66
94.66
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83.88
81.11
                                                                                                                                                                                                                                                                                                                                                                                                                 | SIDSI/gcgdata/geneseq/geneseqp-embl/AA198.DAT:
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA199.DAT:
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:
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                                                                                                                                                                                                                             Length
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167
167
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                                                                   AAY67853
ABP53542
AAM50901
ABU05504
ABU05887
ABP57498
       AAY67859
AAY67860
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                                                                                                                                                                                                                                                                                            SUMMARIES
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/without alignments
40.730 Million cell updates/sec
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S. aureus peptide
Cyclic peptide SEQ
AgrD-autoinducing
M. tuberculosis an
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Staphylococcus aur
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Protected peptide
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ALIGNMENTS

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24-JUN-1999;
                                          29-DEC-1999.
                                                                       Misc-difference
                                                                                        Key
Modified-site
                                                                                                          Staphylococcus aureus.
                                                                                                                      virulence factor; treatment.
                  24-JUN-1998;
                                                     WO9967286-A2
(UYRQ ) UNIV
ROCKEFELLER.
NEW YORK STATE
                 98US-0103438
                             99WO-US14562
                                                            5
/label= Unknown
                                                                                   /note=
                                                                                              Location/Qualifiers
                                                                            "N-terminal residue forms bond with C-terminal residue to form a cyclic peptide"
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Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;

S. aureus peptide #3 used for bacterial interference.

25-APR-2000 AAY67853;

(first entry)

AAY67853 standard; peptide; 9 AA.

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RESULT 2
ABP53542
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cyclic peptides for
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                                                                                                                                                                                                                                                                                           Cyclic peptide;
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                                               WPI;
                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                   agr response inhibitor
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 Claim
                   New cyclic peptides, infections
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24-JUN-1999;
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                                                                                            (NOVI/)
                                                                                    (JIGG/)
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                                               2002-681366/73
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                                                                                  MUIR T W.
MAYVILLE P.
NOVICK R P.
BEAVIS R.
JI G.
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9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                   GVAAXSSLF 9
 Page 10;
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                                                                Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA;
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                                                                                                                                                                                                                                                                                                               SEQ
                                                                                                                                           98US-090402P
99US-0339511
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                                                                                                                                                                                                                                                                                             Staphylococcus aureus; infection; antibacterial;
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18pp;
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                              useful
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9.3e+05;
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RESULT 3
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The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is a secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. Preferred peptides may have the sequence NH2-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z residue and COOH other than a thioester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgrD-autoinducing cyclic peptide, inhibitor of agr response
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                                                                                                                                                                                                                 Claim 7;
                                                                                                                                                                                                                                                                                  Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection i
                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-170774/22
                                                                                                                                                                                                                                                                                                                                                                                                     Muir TW,
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9; Conserv
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NEW YORK STATE
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infection; therapy; cyclic.
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100.0%;
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RESULT 4
ABU05504
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Matches
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This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polynucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cole
                                                                                                                                                                                                                                                                                                                                                            Identifying and selecting genes for survival or virulence of mycobacteria by a comparative genomic analysis of the sequences Mycobacterium tuberculosis and M. leprae -
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                                                                                                                                                                                                                                                                                                      Claim 17;
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9; Conser
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Query Match Best Local S Matches 7

Similarity 7; Conser

Conservative

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Score 31; DB Pred. No. 25; 0; Mismatches

DB 23;

Length 167;

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RESULT 5
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a marker protein from Mycobacterium tuberculosis and Mycobacterium leprae identified using the method of the invention.
                                  This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polymucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and provent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a marker protein from Mycobacterium tuberculosis and Nycobacterium tuberculosis and represent sequence represents.
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                                                                                                                                                                                                                                                                                                                                            WPI;
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                                                                                                                                                                                                                                                      Claim 17;
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                           identified using
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                                                                                                                                                                                                                                                   Page 748;
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77
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RESULT 6
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                                                                                                                                                                                                                                              ABB57436 to ABB57504 represent mycobacterial amino acid sequences (I) encoded by ABZ71062 to ABZ71130 (II), which are isolated from Mycobacterium tuberculosis. (I) are encoded by genes (II) whose expression is induced or up-regulated during culture of a mycobacterium under conditions defined by a dissolved oxygen tension of at least 10% air saturation measured at 37 plus degrees Celsius, when compared with a dissolved oxygen tension of at least 40% air saturation measured at 37 plus degrees Celsius. (I) and (II) have antibacterial, tuberculostatic and immunostimulant activities, and can be used in vaccines and gene therapy. (I) and (II) can be used for the manufacture of a medicament for treating or preventing a mycobacterial infection. They can also be used for the manufacture of a diagnostic reagent for identifying a mycobacterial infection.
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07-SEP-2001; 2001GB-0021780.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mycobacterial peptide, its fragment, variant or
as vaccine for treating or preventing mycobacterial
diagnostic reagents for identifying such infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-201403/19.
N-PSDB; ABZ71124.
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AAY67859;
                           AAY67859 standard; peptide; 9
                                                                                                                                                                                                                                        mycobacterial infection.
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                                                                                                                                                     Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus AgrDII derived peptide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-147202/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-1998;
                                                                                                                                                                                                                                                                                                                      Staphylococcus
                                                                                                                                                                                                 Staphylococcus
                                                                                                                                                                                                                                                  virulence factor.
                                                                                                                                                                                                                                                                                                                                                                        25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY67860 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYRQ ) UNIV ROCKEFELLER.
     24-JUN-1998;
                                                 24-JUN-1999;
                                                                                                   29-DEC-1999
                                                                                                                                                  WO9967286-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ψ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GVAAXSSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVNAASSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0103438
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                                                                                                                                                                                                                                                                          aureus
                                                                                                                                                                                                                                                                                                                      aureus AgrDII derived peptide sequence.
     98US-0103438
                                                    99WO-US14562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.1%;
                                                                                                                                                                                                                                                                          infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 21;
Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infections with Staphylococcus aureus
                                                                                                                                                                                                                                                                          AgrD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Į.
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                                                                                                                                                                                                                                                                            response; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
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Query Match
Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM50907 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Examples; Page 22; 37pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cyclic peptides for treating infections with Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-147202/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muir TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYRQ )
                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protected peptide used in cyclic peptide production.
                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                       Modified-site
24-JUN-1998;
                              24-JUN-1999;
                                                                                            US6337385-B1
                                                            08-JAN-2002
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UNIV NEW YORK STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVAAXSSLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                 aureus; AgrD; agr response; inhibitor; antibiotic;
infection; therapy; cyclic.
98US-090402P
                              99US-0339511
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                         /note=
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77.8%;
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                                                                                                                                                                                                                      "Ser(Bzl)"
                                                                                                                                                                                                                                                       "Ser(Bzl)"
                                                                                                                                                                                                                                                                                       "Ser(tBu)"
                                                                                                                                                                                                                                                                                                                      "Z-Gly"
                                                                                                                         "note linked
peptide"
                                                                                                                                                                                         "note linked
                                                                                                                                                                        peptide"
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Pred. No. 9.3e+05;
0; Mismatches 2
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В

24-JUN-1999;

99US-0339511

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RESULT 10
AAM5102
ID AAM51
XX AAM51
AC AAM51
XX 08-MA
DT 08-MA
XX AgrD2
XX O8-37
PD 08-37
PD 08-37
PD 08-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AAM50899-906). The peptide corresponds to the CC that it is that of a great agreement with a Cys5 to Ser mutation (lactone). It was synthesised on a Wang-resin using an Fmoc N-alpha protection strategy. Following chain assembly, the peptide corresponds to the support and the Ser's residue deprotected by treatment with a trifluoroacetic acid anisole:water mixture (90:5:5) for 4 hr. The partially protected peptide-alpha carboxylates were then dissolved in DMF and treated with PyBOP complete after 2 hr. The remaining protecting groups were then cremoved by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the agr response of CR Staphylococcus aureus. The thiololactone structure within native Replacement of the thiol ester component of the cyclic ring inhibitory activity. The cyclic peptides are useful for centuring inhibitory activity. The cyclic peptides are useful for infaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muir TW, Mayville P,
                                                                                                                                                                Synthetic
                                                                                                                                                                                  Staphylococcus
                                                                                                                                                                                                            AgrD2; agr response; infection; therapy.
                                                                                                                                                                                                                                                          AgrD2 linear thioester peptide
                                                                                                                                                                                                                                                                                         08-MAY-2002
                                                                                                                                                                                                                                                                                                                        AAM51002;
                                                                                                                                                                                                                                                                                                                                                   AAM51002 standard; Peptide; 9 AA
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(UYNY ) UNIV NEW YORK STATE.
                                                                         US6337385-B1
                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVAAXSSLF 9
                                                                                                                                                                                                                                                                                                                                                                                                                               GVNASSSLF
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                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                  aureus
                                                                                                                                  Location/Qualifiers
                                                                                                        /note= "C-terminal thioester"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.1%;
                                                                                                                                                                                                                              inhibitor; antibiotic; antibacterial;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23; I
9.3e+05;
hes 2;
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RESULT 11
AAM51003
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of a novel synthetic AgrD2 linear thioester peptide. The peptide is derived from the cyclic AgrD2 peptide of Stabhylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the garpathetic peptide was assayed using cultured S. aureus strains containing a bera-lactamase reporter gene fused to the agr3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone cyclic peptide (see AAM51001), the present peptide was unable to either activate or inhibit the agr response, even when added to cultured calls at uM concentrations. The invention when added to cultured calls at uM concentrations. The invention of the monitored spectrophotometrically between the peptides are useful for bacterial interference, especially for the treatment of S. aureus
               Muir TW,
                                                                                                                                                        US6337385-B1
                                                                                                                                                                                 Staphylococcus aureus Synthetic.
                                                                                                                                                                                                                     AgrD2; agr response; infection; therapy.
                                                                                                                                                                                                                                                           AgrD2 linear free acid peptide.
                                                                                                                                                                                                                                                                                       08-MAY-2002
                                                                                                                                                                                                                                                                                                                                         AAM51003 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel synthetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-170774/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYRQ )
                                                                            24-JUN-1998;
                                                                                                     24-JUN-1999;
                                                                                                                               08-JAN-2002
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                                     (UYRQ ) UNIV ROCKEFELLER.
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                                                                                                                                                                                                                                                                                                                                                                                                           _
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GVAAXSSLF 9
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             Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mayville P,
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NEW YORK STATE.
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                                                                            98US-090402P
                                                                                                     99US-0339511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.1%;
                                                                                                                                                                                                                                   inhibitor; antibiotic; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novick RP,
             Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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. 9.3e+05;
tches 2;
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RESULT 12
AAM51004
ID AAM51
XX AAM51
AC AAM51
XX AGTD2
XX US633
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                free acid peptide. The peptide is derived from the cyclic AgrD2 coperated of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrP3 promoter. This allowed activation or inhibition of the agr response to be monitored spectropometrically. Unlike an AgrD2 thiololactone cyclic peptide (see AAMS1001), the present peptide was unable to either activate or inhibit the agr response, even when added to cultured cells at uM concentrations. The invention when added to cultured cells at uM concentrations. The invention and methods for preparing them. The cyclic peptides are useful for infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of a novel synthetic AgrD2 linear free acid peptide. The peptide is derived from the cyclic AgrD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection i
                                                                                                         24-JUN-1998;
                                                                                                                                                  24-JUN-1999;
                                                                                                                                                                                           08-JAN-2002
                                                                                                                                                                                                                                                                                                                       Misc-difference 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stpahylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; lactone; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AgrD2 lactone cyclic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM51004 standard; Peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Column 9; 18pp; English
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                                         (UYRQ ) UNIV ROCKEFELLER. (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                       US6337385-B1
                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVAAXSSLF
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                                                                                                           98US-090402P
                                                                                                                                                    9908-0339511
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.1%;
77.8%;
                                                                                                                                                                                                                                                                            "note linked to peptide"
                                                                                                                                                                                                                                                                                                                                       "note linked to peptide"
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Pred. No. 9.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                  residue 5
                                                                                                                                                                                                                                                                                                                                                                   residue 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 9;
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Muir TW,

Mayville P,

Novick RP,

Beavis R,

J.

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RESULT 13
ABB07160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of a novel synthetic AgrD2 lactone cyclic peptide in which residue 5 of the peptide is derived if linked to residue 9 via a lactone bond. The peptide is derived from an AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamese reporter gene fused to the agrP3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. The lactone AgrD2 peptide inhibited the agr response of group I S. aureus strains without activating the agr response of group I I or III strains. The invention provides claimed cyclic peptides (see AAM50899-906 and AAM50899) and methods for preparing them, especially peptides where the cyclic bond is a lactam or lactone bond. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                              Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB07160 standard; peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Column 9; 18pp; English
Use of autoinducer-2 agonists or antagonists autoinducer-2 receptor, regulating bacterial
                                             WPI; 2002-075235/10
                                                                                                                     (UYPR-)
                                                                                                                                                                10-MAY-2000; 2000US-203000P
07-DEC-2000; 2000US-254398P
                                                                                                                                                                                                            10-MAY-2001; 2001WO-US15221.
                                                                                                                                                                                                                                                                       WO200185664-A2
                                                                                                                                                                                                                                                                                                                                vulnerary; pheromone; agr system; accessory gene regulator; cyclic.
                                                                                                                                                                                                                                                                                                                                                                          Peptide-mediated quorum sensing inhibitor peptide cyclo-XII.
                                                                                                                                                                                                                                          15-NOV-2001
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UNIV TE
                                                                                                                     UNIV PRINCETON
QUOREX PHARM II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVNASSSLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                          Dammel
                                                                                                       EX PHARM INC.
TECHNOLOGIES INT INC
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cyclic AgrD-autoinducing peptide for bacterial for treating Staphylococcus aureus infection in a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.1%;
77.8%;
                                                                        Schauder S,
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Pred. No. 9.3e
0; Mismatches
                                                                           Shokat
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9.3e+05;
for regulating activity growth and pathogenesis.
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RESULT 14
ABG15689
ID ABG157
XX ABG15
XX ABG15
XX ABG15
XX Humar
XX Humar
XX Homo
XX Clai
XX The
CC Poly
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Synergistic antibiotic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to or did wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           also antibiotic compositions
                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #15680
                                                                                                                                                                                        diagnostics, forensics, responsible for genetic
                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG15689;
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                                                                                                                                                                           biodiversity
                                                                                                                                                                                                                                                                        N-PSDB; AAS79876.
                                                                                                                                                                                                                                                                                                                                Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WC200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                             2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVAAXSSLF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 AA;
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                                                                                                                                                                                                                                                                                                                                Liu C,
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Pred. No. 9.3e+05;
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Gaps

0

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques

Claim 20; SEQ

ID No 46048; 103pp; English.

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RESULT 15
AAY33146
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Best Local S
Matches 7
This invention describes a novel rabbit carboxylesterase polypeptide (I) capable of metabolizing a chemocherapeutic prodrug and its inactive metabolites into an active drug. The invention also describes a composition comprising (I) and a disease-specific responsive promoter. This composition is useful for sensitizing tumor cells to a chemotherapeutic prodrug (preferably CRT-11 or APC) by transfecting into tumor cells, and contacting the sensitized cells with a chemotherapeutic prodrug to inhibit growth of the tumor cells. The composition can also be administered to the site of tumor resection to inhibit tumor recurrence, and be administered to bone marrow cells to remove tumor cells. The products of the invention are useful for identifying drugs that are inactivated by a carboxylesterase enzyme, and are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carboxylesterase; rabbit; liver; tumour cell; chemotherapy; prodrug; disease-specific responsive promoter; CRT-11; APC; resection; recurrence; inhibition; bone marrow cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rabbit liver carboxylesterase protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY33146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 63-65; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New carboxylesterase polypeptide for treatment of tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-540311/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Danks MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potter PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JUDE CHILDREN'S RES HOSPITAL.
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 2
Pred. No. 6.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .·
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                                                                                      Sequence
                                                                                                                       identifying compounds containing a COOC ester linkage that are activated by a carboxylesterase enzyme. This sequence represents a rabbit liver carboxylesterase fragment which is described in the method of the
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GVALLSSLF
                   GVAAXSSLF
                                                                                         543 AA;
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77.8%;
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Pred. No. 1.
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1.5e+02;
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Search completed: January Job time : 36.0735 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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ALIGNMENTS

Giardia intestinalis

RESULT 1 T18528

probable pyruvate (flavodoxin) dehydrogenase (EC 1.2.99.-) - Giardia intesti
NyAlternate names: pyruvate:ferredoxin oxidoreductase
C;Species: Giardia intestinalis
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
C;Accession: T18528
R;Townson, S.M.; Hanson, G.R.; Upcroft, J.A.; Upcroft, P.
Bur. J. Blochem. 220, 439-446, 1994
A;Title: A purified ferredoxin from Giardia duodenalis.
A;Reference number: S42359; MUID:94170792; PMID:B125101
A;Accession: T1858
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1253 <TOWs
A;Cross-references: EMBL:L27221; NID:g960281; PID:g960283; PIDN:AAA74894.1

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conserved hypothetical protein ML1255 [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Sate: 20.Apr-2001 #sequence_revision 20.Apr-2001 #text_change 10-May-2001 C;Accession: A87066 R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
Na
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A;Molecule type: DNA
A;Residues: 1-163 <STO>
A;Cross-references: GB:AL450380; NID:g13093193; PIDN:CAC31636.1; GSPDB:GN00147
A;Cross-references: GB:AL450380; NID:g13093193; PIDN:CAC31636.1; GSPDB:GN00147
C;Genetics:
A;Gene: ML1255
A;Gene: ML1255
C;Superfamily: Mycobacterium leprae hypothetical protein MLCB1610.16
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A;Residues: 1-167 <COL>
A;Cross-references: GB:AL021246; GB:AL123456; NID:g3261507; PIDN:CAA16045.1; PID:g279150
A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Rv2468c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 28-Ju1-2000
C;Accession: C70866
R;Cole, S.T.; Brosch, R; Parkhill, J; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Cole, S.T.; Brosch, R; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Connor, R; Davies, R; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, SRajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
translocation lipoprotein J
C;Species: Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                                                                                              R;James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, March 1999
A;Reference number: Z22949
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ypothetical protein MICB1610.16 [imported] - Mycobacterium leprae
iSpecies: Mycobacterium leprae
jSpecies: Mycobacterium leprae
jDate: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 28-Jul-2000
jAccession: T45243
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Pred. No. 7.6;
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A,Cross-references: EMBL:AF053946; NID:g2996222; PIDN:AAC62607.1; PID:g2996284
A,Experimental source: strain KIM
R,Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R
Infect. Immun. 66, 4611-4623, 1998
A,Title: DNA sequencing and analyseis of the low-Ca2+-response plasmid pCDl of Yersini
A,Reference number: 222273; MUID:98427122; PMID:9746557
A,Accession: T42861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virC-region lipoprotein yscJ (YlpB) - Yersinia enterocolitica plasmid pYV
C;Species: Yersinia enterocolitica
C;Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 17-Mar-2000
C;Accession: A40049
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                                                                                                                                C; Superfamily: invasin secretion facto C; Keywords: lipid binding; lipoprotein
                                                                                                                                                                                                                                                        A;Reference number: A40361; MUID:91317716; PMID:1860816 A;Accession: A40049
                                                                                                                                                                                                                                                                                             R;Michiels, T.; Vanooteghem, J.C.; Lambert de Rouvroit, J. Bacteriol. 173, 4994-5009, 1991
A;Title: Analysis of virC, an operon involved in the sec
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A; Residues: 1-244 < PER >
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A; Residues: 1-244 < HUP>
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                                                                                                                                                                                                                                 A; Molecule type: DNA
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GVAASASVF
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conserved hypothetical protein PA0340 [imported] - C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 C;Accession: B83602 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Fc

Coulter, S.N.; Folger, K.R.; Kas,

P.; Hickey, M.J.; A.; Larbig, K.; L

#text_change

01-Mar-2002

Pseudomonas aeruginosa

(strain

PAC

RESULT B83602

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C;Accession: AC2730
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, 7; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
                                    A; Molecule type: DNA
A; Residues: 1-305 < KUR>
                                                                                          A; Title: Genome Sequence of A; Reference number: A97359; A; Accession: D97511
                                                                                                                                                 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, I
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.;
Science 294, 2323-2328, 2001
                                                                                                                                                                                                          probable integral membrane protein. (AL132674) [imported] - Agrobacterium to Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C; Accession: D97511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58 A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Accession: AC2730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Karp, P.; Romero, P.; Science 294, 2317-2323, 2A;Authors: Yoo, H.; Tao, Ster, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein Atu1248 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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A;Title: Complete genome sec
A;Reference number: A82950;
                                                                          A; Status: preliminary
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                    Cross-references: GB:AE007869;
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50; MUID:20437337; PMID:10984043
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87.5%;
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66.7%;
                                                                                                               the Plant Pathogen and Biotechnology Agent Agrobacterium MUID:21608551; PMID:11743194
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Pred. No.
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                  PIDN:AAK87045.1; PID:g15156295; GSPDB:GN00169
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Pred. No. 23;
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Markelz, B.,
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F;32-526/Domain: cholinesterase homology <CHE>
F;61,363/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;195,441/Active site: Ser, His #status experimental
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A;Residues: 1-71;193-208;436-446;532-539 <OZO>
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endplasmic reticulum; glycoprotein
                                                                                                                                                                                                                                                                                             A;Reference number: A;Accession: A29471
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 08-Dec-1988 #sequence_revision
C;Accession: A29923; A29471
R;Korza. G; Ozols. J.
J. Biol. Chem. 263, 3486-3495, 1988
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carboxylesterase
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A;Map position: ci
RESULT 11
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A; Residues: 1-539 < KOR>
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A;Accession: A29923
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, MUID:88139431; PMID:3343253
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PMID:3667634
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E64399

hypothetical protein MJ0797 - Methanococcus January Protein MJ0797 - Juli-2000 C;Secies: Methanococcus January Protein Methanococcus January Protein Mile City Protein Methanococcus January Protein Mile City P
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: E64399
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA A;Residues: 1-367 <BUL>
                                                            Query Match
Best Local
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Conservative
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s: GB:U67524; GB:L77117; NID:g2826321;
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87.5%;
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Pred. No.
Mismatches
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Indels
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GVAAXSSL

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R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Xi, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997

J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Recession: C69224

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
aldolase C - chicken (fragment)
C.Species: Gallus gallus (chicken)
C.Date: 04-Sep-1997 #sequence_revision
C.Accession: I51291
C.Accession: I51291
C.R.Meighan-Mancha, R.L.; Tolan, D.R.
J. Cell. Biochem. 57, 423-431, 1995
A.Title: Noncoordinate changes in the s
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A; Residues: 1-1668 < MTH>
A; Residues: 1-1668 < MTH>
A; Cross-references: GB: AE00086B; GB: AE000666; NID: 92622025;
A; Experimental source: strain Delta H
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A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: F85056
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A; Residues: 1-398 <STO>
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Search completed: January 29, Job time: 12.1176 secs

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14:58:21

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AgrD protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Accession: C89995
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, T.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Xobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 125-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89995
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A;Accession: I51291
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: I-42 MEI>
                                                                                                                                   A;Cross-references: GB:BA000018; PID:g13701831; PIDN:BAB43124.1; GSPDB:GN00149 A;Experimental source: strain N315 C;Genetics: A;Gene: agrD
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C89995
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Gapop 10.0 , Gapext 0.5
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  SwissProt_41:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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YSCU YEREN
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Q8k4v2
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4 neisseria m
7 escherichia
9 homo sapien
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01-JUL-1993
15-SEP-2003
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J. Bacteriol .174:3355-3363(1992).

J. Bacteriol .174:3355-3363(1992).

J. Bacteriol ... The EXPORT PROCESS OF THE YOP PROTEINS.

-!- FUNCTION: REQUIRED FOR THE EXPORT PROCESS OF THE YOP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIEST PRESENT STRAIN=CO-92 / Biovar Orientalis; PLASMID=pCD1; MEDLINE=21470413; PubMed=11586360; Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Prentice M.B., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamiln N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague."; Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SPECIES=Y.pseudotuberculosis; STRAIN=YPIII; PLASMID=pIB1;
SPECIES=Y.pseudotuberculosis; STRAIN=YPIII; STRAIN=YPIII; PLASMID=PIB1; STRAIN=YPIII; STRAIN=YPIII; STRAIN=YPIII; STRAIN=YPIII; STRAIN=YPIII; STRAIN=YPIII; STRAIN=YPIII; STRAIN=YPIII; STRAIN=YPIII; STRAIN=YPIII
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15-SEP-2003 (Rel. 42, Last annotation update)
YOP proteins translocation lipoprotein J precursor (Lipoprotein ylpB)
(Low calcium response locus protein KA).
YSCJ OR YLPB OR LCRKA OR YPCD1.59 OR Y5019 OR Y0022.
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SPECIES=Y.pestis; STRAIN=KIM5 / B
MEDLINE=98427122; PubMed=9746557;
Perry R.D., Straley S.C., Fethers
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YSCJ OR YLPB OR LCRKA CR YPCD1.59 OR Y5019 OR Y
Yersinia pestis, and
Yersinia pseudotuberculosis.
Plasmid pCD1, and Plasmid pIB1.
Bacteria; Proteobacteria; Gammaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "DNA sequencing and analysis of Yersinia pestis KIM5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perry R.D., St
Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacteriaceae; Yersinia.
NCBI_TaxID=632, 633;
                                                                                                                                                                                                                                         -!- INDUCTION: At 37 degrees Celsius in the absence of calc
-!- SIMILARITY: BELONGS TO THE YSCJ FAMILY OF LIPOPROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.J.,
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Best Local S
Matches
InterPro, IPR0003/3,
InterPro, IPR0003/3,
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B_2; 1.
PROSITE; PS00941; CARBOXYLESTERASE B_2; 1.
Glycoprotein; Hydrolase; Serine esterase; E:
Glycoprotein; 195
195
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SIMILARITY
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BY SIMILARITY
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EMBL; AF053946; AAC62607.1; -.
EMBL; AL17189; CAB54936.1; -.
EMBL; M83986; AAAZ77551.1; -.
PIR; T43566; T43566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation and characterization of a 60-kilodalton glycoprotein esterase from liver microsomal membranes.";
J. Biol. Chem. 262:15316-15321 | membranes.";
-i- PUNCTION: INVOLVED IN THE DETOXIBICATION OF XENOBIOTICS AND THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
-I- CATALYTIC ACTIVITY: A carboxylic ester + H(2)0 = an alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1989 (Rel. 12, Created)
01-FEB-1991 (Rel. 17, Last sequence up.
28-FEB-2003 (Rel. 41, Last annotation.
Liver carboxylesterase 1 (EC 3.1.1.1).
Oryctolagus cuniculus (Rabbit).
Enternation (Research (Re
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01-OCT-1989
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                     InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs_site.
                                                                                                                                                                                                                                                                                                                                                                                      PIR; A29923; A29923.
HSSP; P21836; 1MAH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to

    -!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ozols J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carboxylic anion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263:3486-3495(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=3667634;
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Pred. No.
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MEDLINE=96337999; pubMed=888087;

Bult C.J., White O. Obsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Xlenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997
01-NOV-1997
16-OCT-2001
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Y797_!
                                                                     TRANSMEM SEQUENCE
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                                                                                                                                                                                                                                                                                                                                     jannaschii.";
Science 273:1058-1073(1996).
                                                                                                                                                                  EMBL; U67524; AAB98792.1; PIR; E64399; E64399. TIGR; MJ0797; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
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TRANSMEM
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Uprotein MJ0797.
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QBRFL1;
28-FEB-2003 (Re
28-FEB-2003 (Re
15-SEP-2003 (Re
Hydroxylamine r
HCP CR FN0684.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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-!- COFACTOR: Binds 2 Fe/S clusters: 1 4Fe-4S cluster 4Fe-20-2S cluster (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the HCP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 25586;
MEDLINE=21886394; PubMed=11889109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; Metal-binding; Iron; Iron-sulfur;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03063; Prismane;
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STRAIN=ATCC 25586
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Bacteria; Fusobacteria;
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ro; IPR004137
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(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
re reductase (EC 1.7.-.-) (Hybrid-cluster protein)
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                    IRON-OXO-SULFUR (4FE-20-2S)
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., Zhu L.,
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ZW-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 4-hydroxythreonine-4-phosphate dehydrogenase (EC (phosphohydroxy)-1-threonine dehydrogenase).
OS PDXA OR XF0839.
OS Xylella fastidiosa.
CB Bacteria; Proteobacteria; Gammaproteobacteria; Xan X CBI_TaxID=2371;
V (1)
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PDXA_XYLFA
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Transmembrane;
TRANSMEM 25
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01-NOV-1995
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000609; :
Pfam; PF02118; Srg; 1
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STRAIN=Bristol N2;
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(Rel. 32, Last sequence update)
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                                                                                                                                                                                                                                                                      Score 28;
Pred. No.
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MBL outstation -
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RESULT 8
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AC Q41629
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RA ALVARENDA R.J. Reinach F. C., Arruda F. Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptissa C.S.,
RA Barros M.H., Balocorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto M.R.P., Camargo A.A., Camargo L.B.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.E., Costa M.C.R., Costa Neto C.M.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Fromme M., Furlan L.R.,
RA Fraga J.S., Jouldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Macchado J.A.,
RA Marques M.V., Martins E.A., Lopes C.R., Marino C.L.,
RA Marques M.V., Martins E.A., Lopes C.R., Marino C.L.,
RA Marques M.V., Martins E.A., Lopes C.R., Marino C.L.,
RA Marques M.V., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Marques M.V., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Menck C.P.M., Miracca E.C., Myaki C.Y., Monteiro-Vitcrello C.B.,
RA Menck C.P.M., Miracca E.C., Nunes L.R., Oliveira M.A.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Solva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA de Solva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Zago M.A., Zatz M., Weidanis J., Setubal J.C.;
RI Time genome sequence of the plant pathogen Xylella fastidiosa.";
RA Zago M.A., Zatz M., Weidanis J., Setubal J.C.;
Inhosphohydroxy) butyric acid which spontaneously decarboxylate to C. phosphohydroxy) butyric acid which spontaneously decarboxylate to Company threenine + NADH.
                                                                                                                                                                                                 Query Match
Best Local S
Matches 7
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STRAIN=9a5c;
MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                               Pfam; PF04166; PdxA; 1.
TIGRPAMS; TIGR00557; pdxA; 1.
Pyridoxine biosyntheeis; Oxidoreductase; NAD; Complete proteome.
SEQUENCE 330 AA; 34553 MW; A981237FCB44CF71 CRC64;
                                                                                                                                                                                                                                                                                                                                                              EMBL; AE003923; AAF83649.1; PIR; D82756; D82756. HAMAP; MF_00536; -; 1. InterPro; IPR005255; PdxA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pyridoxal phosphate.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: BELONGS TO THE PDXA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino-3-oxo-4-phosphonooxybutyrate + NADH. PATHWAY: De novo synthesis of pyridoxine (vitamin
                                                                                                                      302
                                                                                                                                                                                                   Similarity 7; Conserv
                                                                                                                      GVADPSSLF 310
                                                                                                                                                             GVAAXSSLF 9
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                       75.7%;
                                                                                                                                                                                             0;
                                                                                                                                                                                                                     Score 28;
Pred. No.
                                                                                                                                                                                                   Pred. No. 36;
); Mismatches
                                                                                                                                                                                                                       DB 1;
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ADT1_WH Q41629;

WHEAT

PRT;

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Best Local S
Matches
                                              15-JUL-1998 (Rel
15-JUL-1998 (Rel
16-OCT-2001 (Rel
ADP,ATP carrier p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triticum aestivum (Wheat).
Tukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein 1, mitochondrial precursor translocase 1) (Adenine nucleotide translocator 1)
                                                                                                          ADT2
                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00926; MITCCARRIER.
PROSITE; PS00215; MITCCH CARRIER; 2.
Mitcchondrion; Inner membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Leaf;
Iacobazzi V., Poli A., Blanco A., Palmieri F.;
Iacobazzi V., Poli A., Blanco A., Palmieri F.;
"Nucleotide sequences of two genes (ANT-G1 and ANT-G2)
adenine nucleotide translocator of wheat mitochondria."
Eukaryota; Viridiplantae;
                                  translocase
                                                                                             Q41630;
                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X95863; CAA65119.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4565;
          Triticum aestivum (Wheat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: Belongs to the mitochondrial carrier family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: CATALYZES THE EXCHANGE OF MITOCHONDRIAL INNER MEMBRANE. SUBUNIT: Homodimer (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Gene Register PGR96-016.
                                                                                                          WHEAT
                                                                                                                                                                    144
                                                                                                                                                                                                                                                                                                                                                                                                                            PF00153; mito
                                                                                                                                                                                           1 GVAAXSSLF 9
                                                                                                                                                                                                                  6; Conserv
                                                                                                                                                                                                                                                                                                                                                                           peptide;
                                                                                                                                                                     GAAGASSLF 152
                (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
(Rel. 40, Last intochondrial precursor protein 2, mitochondrial precursor 2)
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140
201
240
296
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                                                                                                                                                                                                                                                                   AA;
                                                                                                          STANDARD
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220
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314
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66.7%;
Streptophyta; Embryophyta; Tracheophyta;
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Pred.
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1 (POTENTIAL).
2 (POTENTIAL).
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36;
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                                                                                                                                                                                                                                         Length 331;
                                                                                                                                                                                                                                                                   CRC64;
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                                 (ADP/ATP (ANT 2).
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RESULT 10
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ID SFUA
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AC P2144
AC P2144
AC P2147
DT 01-M
DT 15-U
DT 11-U
DT 11-
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Best Local
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01-MAY-1991 (Rel. 18, C

01-MAY-1991 (Rel. 18, L

15-JUL-1999 (Rel. 38, L

Iron(III) -binding perip
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        SERMA
SFUA_
transport
  Angerer A., Gaisser S., Braun V.; "Nucleotide sequences of the sfuA, sfuB, and sfuC genes of marcescens suggest a periplasmic-binding-protein-dependent transport mechanism.";
                                                                                                                                                                  Bacteria; Proteobacteria;
Enterobacteriaceae; Serra
                                                                                                                                                                                                           Serratia marcescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch carrier.
Pfam; PF00153; mitocarr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH CARRIER; 2.
Mitochondrion; Inner membrane; Repea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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"Mucleotide sequences of two genes (ANT-G1 and ANT-G2) e
adenine nucleotide translocator of wheat mitochondria.";
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Triticeae; Triticum.
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TISSUE=Leaf;
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                                                                            WEDLINE=90130288; PubMed=2404942;
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                                                                                                       EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) Plant Gene Register PGR96-01
FUNCTION: CATALYZES THE EXCHI
MITOCHONDRIAL INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Homodimer
                                                                                                                                                                                                                                                                                                                                                        SERMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide; Multigene
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                                                                                                                                                                    Serratia
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Last annotation updat
                                                                                                                                                                                                                                                                                                                Created)
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NN: Integral memb
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THE EXCHANGE OF
                                                                                                                                                                                      Gammaproteobacteria; Enterobacteriales;
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Pred. No. 36;
0; Mismatches
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ADP, ATP CARRIER |
1 (POTENTIAL).
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4 (POTENTIAL).
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ı precursor.
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(See http://www.isb-sib.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 331;
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tent is in no
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RESULT
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Best Local S
Matches 5
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TISSUE=Fibroblast;
MEDLINE=87161904; P.
IZZO P., COStanzo P
HUMAN
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-I- FUNCTION: INVOLVED IN A PERIPLASMIC BINDING-PROTEIN-DEPENDENT IRON TRANSPORT SYSTEM, WHICH IS INDEPENDENT OF TONE, EXBE, SIDEROPHORE, OR ANY OUTER MEMBRANE PROTEIN. HOWEVER, IT IS NOT CLEAR HOW FE(III) IS SOLUBILIZED AND TAKEN UP ACROSS THE OUTER
                                                                                                                                                                                                                                                                                              "A new human species
"A new hiochem. 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1986 (Rel. 03, Created)
01-APR-1988 (Rel. 07, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Fructose-bisphosphate aldolase A (EC 4
(Lung cancer antigen NY-LU-1).
ALDOA OR ALDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transport;
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01-NOV-1986
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                                                                                                                                 MEDLINE-88271327; PubMed=3391172;
Izzo P., Costanzo P., Lupo A., Rippa E., Paolella G., Salvatore F.;
"Human aldolase A gene. Structural organization and tissue-specific expression by multiple promoters and alternate mRNA processing.";
Eur. J. Biochem. 174:569-578(1988).
                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=88271327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR006061;
Pfam; PF01547; SBP_ba
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HSSP; P35755; 1MRP.
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1 26 POTENTIAL.
27 338 IRON(III)-BINDING PERIPLASMIC
27 338 AA; 36157 MW; DD5FAA452301A716 CRC64;
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P., Lupo A., Ri
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Primates;
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) THE BACTERIAL
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Catarrhini;
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i; Hominidae;
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VARIANT HEMOLYTIC ANEMIA GLY-128.

MEDLINE-91035340; PubMed-2229018;

Takasaki Y., Takahashi I., Mukai T., Hori K.;

"Human aldolase A of a hemolytic anemia patient with substitution: characteristics of an enzyme generated transfected with the expression plasmid pHAAD128G.";
                                                                                MEDIINE=88068641; PubMed=2825199;
Kishi H., Mukai T., Hirono A., Fujii H., Miwa S., Hori K.
"Human aldolase A deficiency associated with a hemolytic
thermolabile aldolase due to a single base mutation.";
proc Natl. Acad. Sci. U.S.A. 84:8623-8627(1987).
                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINB=99156067; PubMed=1004832;
Dalby A., Dauter Z., Littlechild J.A.;
Crystal structure of human muscle aldolase
"Crystal structure of human muscle aldolase
1,6-bisphosphate: mechanistic implications."
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88046782; PubMed=3674018;
Tolan D.R., Niclas J., Bruce B.D., Lebo
"Evolutionary implications of the human
pseudogene chromosome locations.";
Am. J. Hum. Genet. 41:907-924(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Freemont P.S., Dunbar B
"The complete amino aci-
bisphosphate aldolase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91153319; PubMed=1999195;
Mukai T., Arai Y., Yatsuki H., Joh
"An additional promoter functions i
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Gamblin S.J., Dav.
Littlechild J.A.,
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MEDLINE=90242948; PubMed=2335208;
Gamblin S.J., Cooper B., Millar J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maire P., Gautron S., Hakim V., Gree
"Characterization of three optional
human aldolase A gene.";
J. Mol. Biol. 197:425-438(1987).
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Freemont P.S., Dunbar B., Fothergill L.A.;
"Human skeletal-muscle aldolase: N-terminal sequen
CNBr- and o-lodosobenzoic acid-cleavage fragments.
Trih. Blochem. Blophys. 228:342-352(1984).
                                                                                                                                   MEDLINE=88068641; PubMed=2825199;
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PubMed=3441006;
S., Hakim V., Gregori
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nbar B., Fothergill-Gilmore L.A.;
no acid sequence of human skeletal-muscle
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EMBL; X05236; CAA28861.1; -.
EMBL; M11560, AAA51690.1; -.
EMBL; M1560, AAA51690.1; -.
EMBL; X12447; CAA39979.1; ALT_SEQ.
EMBL; M21190, AAA51697.1; -.
PIR; S14084; ABHUA.
PDB; 1ALD; 15-APR-92.
PDB; 2ALD; 20-APR-99.
PDB; 4ALD; 02-MAR-99.
PDB; 4ALD; 02-MAR-99.
AARTHUS/Ghent-2DPAGE; 1302; NEPHGE.
Siena-2DPAGE; P04075; -.
                                                                                                                                                                                                                                                         Disease mutation.
INIT MET 0
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BINDING 229
ACT_SITE 363
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BINDING
ACT_SITE
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GK; P04075; -.

GK; P04075; -.

GO; GO:0004332; F:fructose-bisphosphate aldolase activity;

GO; GO:0006000; P:fructose metabolism; TAS.

GO; GO:0006096; P:glycolysis; TAS.

GO; GO:0006941; P:striated muscle contraction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biochem. 108:153-157(1990).

-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = gphosphate + D-glyceraldehyde 3-phosphate.

-!- PATHMAY: Glycolysis; sixth step.

-!- SUBUNIT: Homotetramer.

-!- DISEASE: Defects in ALDOA are a cause of hemolytic
                                                                                                                                                                                                                                                                                                                          InterPro; IPR000741; Aldolase_I.
Pfam; PF00274; glycolytic_enzy; 1.
ProDom; PD001128; Aldolase_I; 1.
PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
Lyase; Schiff base; Glycolysis; Multigene
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SIMILARITY: Belongs to class I fructose-bisphosphate aldolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [MIM:103850]
                                                                                                                                                                                                                           128
 C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
SCHIFF-BASE WITH DIHYDROXYACETOMEP.
ESSENVIAL FOR ENHANCED ACTIVITY OF THE
ENZYME TOWARD FRUCTOSE 1,6-BISPHOSPHATE
AS COMPARED WITH FRUCTOSE 1-PHOSPHATE
D -> G (in hemolytic anemia;
thermolabile).
/FTId=VAR_000550.
                                                                                                                                                                                                                                                                                                                             family;
                                                                                                                                                                                                                                                                                                                              3D-structure
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aldolase B
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X MEDLINE=88192445; PubMed=3009179;

X MEDLINE=88192445; PubMed=3009179;

X Paolella G., Buono P., Mancini P., Izzo P., Salvatore F.;

XI Denote and expression of mouse aldolase genes. Brain-specific related to aldolase A.";

Y aldolase C amino acid sequence is closely related to aldolase A.";

Y Eur. J. Blochem. 156:229-235(1986)

C -: CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate.

C -: PATHWAY: Glycolysis; sixth step.

C -: SUBUNIT: Homotetramer:

C -: SUBUNIT: Homotetramer:

C -! MISCELLANDOUS: In vertebrates, three forms of this ubiquitous of glycolysic enzyme are found, aldolase A in muscle, aldolase B in color of the col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALFA MOUSE STANDARD; PKT; JoJ Am. 1905064; 13-AUG-1987 (Rel. 05, Created) 01-AUG-1988 (Rel. 08, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Fructose-bisphosphate aldolase A (EC 4.1.2.13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-265 AND 294-363 FROM N.A. MEDLINE=90307699; PubMed=2365699; Stauffer J.K., Colbert M.C., Clejek-Baez "Nonconservative utilization of aldolase J. Biol. Chem. 265:11773-11782(1990).
                                                                                                                                                                                                                                                                                                       MEDLINE-88096598; PubMed-3697100;
Mestek A., Stauffer J., Tolan D.R., Ciej
"Sequence of a mouse brain aldolase A cD!
Nucleic Acids Res. 15:10595-10595(1987).
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=129;
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
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STRAND
TURN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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ALDOA OR ALDO1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAASESLF 357
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Rodentia;
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Sciurognathi; Muridae;
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A cDNA.";
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A alternative
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; Murinae; Mus
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EMBL; J05517; AAA37210.2; -.
EMBL; Y00516; CAA68571.1; -.
PIR; 806323; ADMSA.
HSSP; P00883; 1ADO.
SWISS-2DPAGE; P05064; MOUSE.
                                                                                                                                                   MEDLINE=74094688; PubM
Lai C.-Y., Nakai N., C
"Amino acid sequence o
the active center.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P00883; Q28671;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequents of the control of the contro
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SEQUENCE OF 1-164.
MEDLINE=75145171;
Nakai N., Chang D.
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=84111505; PubMed=6546378; Tolan D.R., Amsden A.B., Putney S. "The complete nucleotide sequence messenger RNA.";
                                                                                            Science 183:1204-1206(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
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m; PF001128; Aldolase I; 1.
TE; PS00158; ALDOLASE_CLASS_I; 1.
TE; Schiff base; Glycolysis; Multigene
MET 0 0 C-1-PHOSPHATE
NG 55 C-1-PHOSPHATE
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      PubMed=1122141;
., Lai C.-Y.;
                                                                                                                                                                                                                                            PubMed=4812352;
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39224 MW;
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229
363
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C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
SCHIFF-BASE WITH DIHYDROXXACETONE-P.
ESSENTIAL FOR ENHANCED ACTIVITY OF THE
ENZYME TOWALD FRUCTOSE 1,6-BISHOSPHATE.
AS COMPARED WITH FRUCTOSE 1-PHOSPHATE.
AS COMPARED WITH FRUCTOSE 1-PHOSPHATE.
S-> C (IN REF. 3).
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4.1.2.13)
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39;
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Blom N., Sygusch J.,

"Product binding and role of the C-terminal region in c

"product binding and role aldolase.";

Nat. Struct. Biol. 4:36-39(1997).

-i. CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = g

phosphate + D-glyceraldehyde 3-phosphate.

-i. PATHWAY: Glycolysis; sixth step.

-i. PATHWAY: Glycolysis; sixth step.

-i. SUBUNIT: TETRAMER OF NEARLY IDENTICAL CHAINS, ALPHA

DIFFER AT ONLY 1 POSITION. N-360 IN THE ALPHA CHAIN.

TO D-360 IN THE BETA CHAIN.

-i. MISCELLANEOUS: In vertebrates, three forms of this

glycolytic enzyme are found, aldolase A in muscle,

liver and aldolase C in brain.

-i. SIMILARITY: Belongs to class I fructose-bisphosphat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in class
J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [5]
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MEDLIND=80109133; PubMed=534504;

Benfield F.A., Forcina B.G., Gibbons I., Perham R.N.;

"Extended amino acid sequences around the active-site lysin of class-I fructose 1,6-bisphosphate aldolases from rabbit sturgeon muscle, trout muscle and ox liver.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=74163196; PubMed=4857186;
Hartman F.C., Welch M.H.;
"Identification of the histidyl residue of rabbit
alkylated by N-bromoacetylethanolamine phosphate.'
Biochem. Biophys. Res. Commun. 57:85-92(1974).
                                                                                                                                                                                                                                                                                                                                                                  SUBSTRATE-BINDING SITE.

MEDILINE-80046697; PubMed-499203;

Patthy L., Varadi A., Thesz J., Kovacs K.;

"Identification of the C-1-phosphate-binding arginine residue of 
"rabbit-muscle aldolase. Isolation of 1,2-cyclohexanedione-labeled 
peptide by Chemisorption Chromatography.";

Eur. J. Biochem. 99:309-313(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Studies on the structure o tryptic peptides; sequence terminal BrCN peptide."; Arch. Biochem. Biophys. 166
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                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1
MEDLINE=97143309; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=76190154; PubMed=5453;
Hartman F.C., Brown J.P.;
"Affinity labeling of a previously
in class I fructose bisphosphate al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 37-55 AND 349-363 FROM MEDLINE=83167564; PubMed=6687628;
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[7]
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MEDLINE=75145172; Pu
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                                                         WWW="http://www.worthington-biochem.com/manual/A/ALD.html".
                                                                           DATABASE: NAME=Worthington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by shotgun sequencing.";
e 302:718-721(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the structure of rabbit muscle aldolase. structure of the COOH-terminal BrCN peptithe subunit polypeptide chain."; the subunit polypeptide chain."; em. Biophys. 166:358-368(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183:429-444(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251:3057-3062(1976)
                                                                                                                                                                                                                                                                                                                      PubMed=8989320;
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PubMed=1122142;
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REMBL; V00876; CAA24245.1; -.

REMBL; V00877; CAA24245.1; -.

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REMBL; V00877; CAA242444.1; -.

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REMBL; V00877; CAA242444.1; -.

REMBL; V00877; CAA24244, ..

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REMBL; V00877; CAA242444.1;

REMBL; V00877; CAA24244, ..

REMBL; V00877; CAA24244, ..

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DIHYDROXYACETONE PHOSPHATE AND
DIHYDROXYACETONE PHOSPHATE AND
C1-PHOSPHATE GROUP OF THE SUBSTRATE,
ALKYLATION INACTIVATES THE ENZYME.
SCHIFF BASE WITH DIHYDROXXACETONE-P.
ALKYLATION INACTIVATES THE ENZYME;
ESSENTIAL FOR THE SUBSEQUENT HYDROLYSIS
OF THE DIHYDROXYACETONE SCHIFF BASE.
ESSENTIAL FOR ENHANCED ACTIVITY OF THE
ENZYME TOWARD FRUCTOSE 1,6-BISPHOSPHATE
AS COMPARED WITH FRUCTOSE 1-PHOSPHATE.
N - D (IN REF. 3).
E-> Q (IN REF. 5).
GOG -> SQE (IN REF. 5).
S -> E (IN REF. 5).
S -> R (IN REF. 6).
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ESSENTIAL FOR CLEAVAGE OF THE SUBSTRATE

TO GLYCERALDEHYDE 3-PHOSPHATE &

DIHYDROXYACETONE PHOSPHATE.

ESSENTIAL FOR CLEAVAGE OF THE SUBSTRATE

TO GLYCERALDEHYDE 3-PHOSPHATE AND
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Matches
                                                           SEQUENCE FROM N.A.

MEDLINE=86083188; PubMed=2416636;

MEDLINE=86083188; PubMed=2416636;

Joh K., Mukai T., Yatsuki H., Hori K.;

"Rat aldolase A messenger RNA: the nucleotide sequence and mRNA species with different 5'-terminal regions.";

Gene 39:17-24(1985).

[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=86140113; PubMed=3753977;
Mukai T., Joh K., Arai Y., Yatsuki H., Hori
"Tissue-specific expression of rat aldolase
species differing only in the 5'-terminal se
J. Biol. Chem. 261:3347-3354(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALFA_RAT STANDARD; PRT; 363 AA. P05065; 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 28-FDB-2003 (Rel. 41, Last annotation update) Fructose-bisphosphate aldolase A (EC 4.1.2.13)
This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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se A mRNAs. Three
sequences.";
                                                                                                      of this ubiquitous muscle, aldolase B
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SEQUENCE FROM N.C.
STRAIN=129/Sv;
Funari V.A., Tolan D.R.;
"Mouse aldolase B (aldo2) genomic sequence of tincluding first poly A site and signals.";
cubmitted (JUN-2001) to the EMBL/GenBank/DDBJ
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Q91Y97; Q8K034; Q91W73;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Fructose-bisphosphate aldolase B (EC 4.1.2.13)
SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE=Colon, Kidney, and Liver;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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HSSP; P00883; 1ADO.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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M14420; AAA40715.1; -.

X04261; CAA27815.1; JOINED.

X04262; CCAA27815.1; JOINED.

X04263; CAA27815.1; JOINED.

X04264; CAA27815.1; JOINED.
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PF00274; glycolytic enzy; 1.
m; PD001128; Aldolase I; 1.
TE; PS00158; ALDOLASE CLASS I; 1.
p; Schiff base; Glycolysis; Multigene family.
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Rodentia;
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C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
SCHIFF-BASE WITH DIHYDROXYACETONE-P.
ESSENTIAL FOR ENHANCED ACTIVITY OF THE
ENZYME TOWARD FRUCTOSE 1,6-BISPHOSPHATE
AS COMPARED WITH FRUCTOSE 1-PHOSPHATE.
AS COMPARED WITH FRUCTOSE 1-PHOSPHATE.
F -> S (IN REF. 2).
M -> V (IN REF. 2).
M4: 48A0468B9E3B9DB8 CRC64;
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Sciurognathi; Muridae;
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Mismatches
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Q91e76 oryza sativ
Q56969 yersinia pe
Q9i6f3 pseudomonas
Q8ufz6 agrobacteri
Q77540 oryccolagus
Q8sva3 encephalito
Q98g45 rhizobium 1
Q9n4s1 caenorhabdi
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Q8sry6 encephalito
Q9cc58 mycobacteri
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Q1-OCT-2002 (TrEMBLrel. 2
Q1-OCT-2002 (TrEMBLrel. 2
Q1-MAR-2003 (TrEMBLrel. 2
Q1-MAR-2003 (TrEMBLrel. 2
Q5JNBA0011L09,21
                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN-CV. Nipponbare;
Buell C.R.; Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Buell C.R.; Yuan Q., Ouyang S., Liu J., Krol M.I., Jarrahi B.B.,
Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
Oryza sativa chromosome 10 BAC OSJNBB0011109 genomic sequence.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                         EMBL; AC092388; AAM22720.1; Gramene; Q8L676; -. InterPro; IPR004843; M-ppes
                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                    Hypothetical SEQUENCE 3.
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Pfam; PF00149; Metallophos; 1.
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MEDIINE=21576510; PubMed=11719806; Katinka M.D., Duprat S., Cornillot E., Mete Prensier G., Barbe V., Peyretaillade E., Br Delbac F., El Alaoui H., Peyret P., Saurin Weissenbach J., Vivares C.P.; "Genome sequence and gene compaction of the Encephalitozoon cuniculi."; Nature 414:450-453 (2001).

EMBL; AL590445; CAD26577.1; -.
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InterPro; IPR005479; CPase_L_D2.
InterPro; IPR002869; POR.
InterPro; IPR002860; POR.N.
Pfam; PF00157; fer4; 2.
Pfam; PF001578; POR; 1.
Pfam; PF01585; POR; 1.
Pfam; PF01855; POR; 1.
PROSITE; PS00167; CPSASE_2; 1.
4Fe-4S; Iron; Iron-sulfur
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Q24382;
Q1.NOV-1996 (TrEMBLrel. 01, Created)
Q1.DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1.DEC-2003 (TrEMBLrel. 23, Last annotation update)
Q1.DEC-2003 (TrEMBLrel. 23, Last annotation update)
Q1.DEC-2003 (TrEMBLrel. 23, Last annotation update)
Q24382;
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EMBL; L27221; AAA74894.1; -.
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NCBL_TaxID=5741;
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Submitted (APR-2001)
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STRAIN=GB-M1;
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VCBI_TaxID=6035;
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(TrEMBLrel. 23, Last annotation updat
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77.8%;
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o the EMBL/GenBank/DDBJ
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Pred.
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Best Local S
Matches
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O53195;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-MR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv2468C.
RV2468C OR MTV008.24C OR MT2543.
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01-JUN-2001
01-JUN-2001
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mingall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simmon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
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Pfam; PF01490; Aa_trans; 1.
Hypothetical protein.
SEQUENCE 385 AA; 43606 M
SEQUENCE FROM N.A. STRAIN=H37RV; MEDLINE=98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leproma; ML1255; -
Hypothetical prote:
SEQUENCE 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Massive gene decay in the leprosy Nature 409:1007-1011(2001). EMBL; AL583921; CAC31636.1; -.
                                                                                                                                            Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium
                                                                                                                       Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium leprae.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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L (TrEMBLrel. 17, 1
L (TrEMBLrel. 18, 1
al protein ML1255.
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     PubMed=9634230,
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16842 MW;
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Last annotation updat
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Pred. No.
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Pred. No. 27;
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F26A1A2C04E3FD2E CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 17.4 kDa protein.
MLCB1610.16.
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Q9X7B5;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seeger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium leprae.
Mycobacteria; Actinobacteridae; Actinomycetales;
Bacteria; Actinobacteria; Actinobacteridae; Mycobacterium.
                                                                                                                                                       MEDLINE=93188700; PubMed=8446027;

Eiglmeier K., Honore N., Woods S.A.,

"Use of an ordered cosmid library to

of Mycobacterium leprae.";

Mol. Microbiol. 7:197-206(1993).

EMBL; AL049913; CAB43162.1; -.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
James K.D., Parkhill J.,
Submitted (MAR-1999) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laboratory strains.";
Submitted (APR-2001) to the EM
EMBL; AL0021246; CAA16045.1; --
EMBL; AB007091; AAK46843.1; --
TIGR; MT2543; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C., III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                          Hypothetical protein. SEQUENCE 169 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1769;
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STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bishai W
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(MAY-1999)
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al protein; Coi
167 AA; 1728
     Conservative
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Q56969;
Q1-NOV-1996
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Q9LE76;
01-OCT-2000
01-OCT-2000
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-2000) to the EMBL/GenBank/DDBJ EMBL; AP001081; BAA90367.1; -. EMBL; AP001073; BAA89586.1; -. Gramene; Q9LE76; -.
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Oryza sativa (Rice).
Cutyas sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
Enterobacteriaceae; Yersir
NCBI TaxID=632;
Filippov A.A.;
Submitted (MAR-1994)
                                                                                                                           Smirnov G.B.;
"Sequencing of two Contrib. Microbiol.
                                                                                                                                                                                                          SEQUENCE OF 142-236
STRAIN=358;
Filippov A.A., Olein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sasaki T., Matsumoto T., "Oryza sativa nipponbare clone:P0693B08.";
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Matsumoto I.,
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RESTRAIN=ATCC 1592 / PAO1;

REMEDILINE=20437337; PubMed=10984043;

REMEDILINE=20437337; PubMed=10984043;

REA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.,

RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

RI Nature 406:959-964 (2000).

DR EMBL, AE004472, AAG03729.1; -.

PRI MELL AE004472, AAG03729.1; -.

PRI NETURE 406:959-964 (2001).
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SEQUENCE FROM N.A.
STRAIN=358;
MEDLINE=92250432; F
Q8UFZ6;
Q8UFZ6;
01-JUN-2002
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CONFLICT
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"A novel protein, LcrQ, involved in the low-calcium response Yersinia pseudotuberculosis shows extensive homology to Yoph.
J. Bacteriol. 174:3355-3363(1992).
BACLETION. 174:3355-3363(1992).
InterPro; IPR003282; SecIIIOMPK.
InterPro; IPR005182; YscJ FiiF.
InterPro; IPR005182; YscJ FiiF.
Pfam; PF01514; YscJ FiiF.
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Hypothetical protein; Complete
SEQUENCE 267 AA; 27809 MW;
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                                                                                                                                                                                                                                           077540 PRELIMINARY; PRT; 565 AA.
077540;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Liver carboxylesterase (EC 3.1.1.1).
Liver carboxylesterase (EC 3.1.1.1).
Oryctolagus cuniculus (Rabbit).
Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Interpro; IFKOULT:
Pfam; PF00892; DUF6; 1.
PROSITE; PS00095; C5 MTASE 2; 1.
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MEDITIME=21608550; PubMed=11743193;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L.

Chen Y., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin G., Rouse G., Saenphimmachak C., W. Z., Romero P., Gordo,

Raymond C., Rouse G., Saenphimmachak C., W. Z., Romero P., Gordo,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Mestry F. W., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cielo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
Science 294:2323-2338(2001)
EMBL; AE009087; AAL42257.1; --
EMBL; AE009087; AAK497045.1; --
InterPro; IPR001525; C5 DNA meth.
InterPro; IPR001520; DUF6.
   TISSUE=Liver;

MEDLINE=99297515; PubMed=9635592;

Potter P.M., Pawlik C.A., Morton C.L., Naeve C.W.,

"Isolation and partial characterization of a cDNA
liver carboxylesterase that activates the prodrug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmfel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C58. "
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-!- SIMILARITY: BELONGS TO THE TYPE-B CARB
EMBL; AF036930; AAC39258.1; -.
HSSP; P21836; IMAH.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR002018; Ser estrs_site.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE_B 2; 1.
                                                                           Q98G45;
Q98G45;
01-OCT-2001
01-OCT-2001
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21576510; PubMed-11719806;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thom
Prensier G., Barbe V., Peyretaillade E., Brottier P., Wi
Delbac F., El Alacui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.;
"Genome sequence and gene compaction of the eukaryote pa
Encephalitozoon cuniculi.";
Nature 414:450-453(2001).
BMBL; AL590446; CAD25457.1; -.
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SEQUENCE
  Rhizobium
                            Iron-binding periplasmic protein,
MLR3495.
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Eukaryota; Fungi; Microsp
NCBI TaxID=6035;
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STRAIN=GB-M1;
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1 (TrEMBLrel.
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(Mesorhizobium loti)
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66.7%;
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77.8%;
                                                                        18, Created)
18, Last sequence update)
23, Last annotation updat
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Pred. No. 1.5e
1; Mismatches
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Pred. No.
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1.7e+02;
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1.5e+02;
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Q9N4S1
IQ Q9N4S1
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Matches 6
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       Matches
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01-0CT-2000
01-MAR-2003
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STRAIN-MARF730309;
MEDIXIN-21082930, PubMed=11214968;
MEDIXIN-21082930, PubMed=11214968;
MEDIXIN-21082930, PubMed=11214968;
MEDIXIN-21082930, FubMed=11214968;
Manabe A., Idésawa Y., Sato S., Asamizu E., Kawashima K., Kimura T.
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto
Takeuchi C., Yamada M., Tabata S.;
Takeuchi C., Yamada M., Tabata S.;
                                                                                        "Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
EMBL; AC006804; AAF60757.1; -.
Wormbep; YS3G8B.4; CE25430.
Hypothetical protein.
SEQUENCE 349 AA; 37676 MW; COE76887720CAOF
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Y53G8B.4.
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InterPro; IPR006059; SBP_bac_1.
Pfam; PF01547; SBP_bac_1; 1.
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Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                    Waterston R.;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                             Latreille P.;
"The sequence of C.
Submitted (MAR-1999)
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode investigating biology. The C. elescience 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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NCBI_TaxID=6239;
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Eukaryota; Metazoa; Nematoda;
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(TIRMBLrel. 15, Last sequence up
(TIRMBLrel. 23, Last annotation
1 37.7 kDa protein.
    Conservative
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66.7%;
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66.7%;
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EMBL/GenBank/DDBJ
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Pred. No. 1.7e
2; Mismatches
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                       Score
Pred.
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       Mismatches
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1.7e+02;
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                                              Length 349;
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GVAAXSSLF

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RESULT 15
Q9XEC:
ID Q9XEC:
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DT 01-NC
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Search completed: January 29, 2004, 14:56:46 Job time : 27.8676 secs
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                                                                                                                                                                                                                                                                                                                  Query Match 78.4%; Score 29; DB 10; Length 398; Best Local Similarity 66.7%; Pred. No. 2e+02; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF076243; AAD29760.1; -.
EMBL; AL161500; CAB77916.1; -.
Hypothetical protein.
SEQUENCE 398 AA; 43961 MW; 0077BE2298E94AD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. Columbia;
STRAIN-CV. (Columbia;
Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y.;
The Columbia sequence of Arabidopsis thaliana BAC T26N6, chromosome
19.3 cM.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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OYEC5;

O1-NOV-1999 (TrEMBLrel. 12, Created)

O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)

O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)

O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)

Hypothetical 44.0 kDa protein.

T26N6.8 OR AT4G04480.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

MCBI TaxID=3702;
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Zhong J., Ma P., Parnell L.D., Chen C.N., Chen E.Y., Mewes H.W.,
Lemcke K., Mayer K.F.X.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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GLAVSSSLF 69
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e 8, Appli e 8, Appli e 8, Appli e 36, Appli e 32874, A e 26, Appl e 28, Appl e 29161, A e 39503, A

17, Appl 2, Appli 227, App 4192, Ap 310, App 1034, Ap 16, Appl 14, Appl 14, Appl

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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seq length: 2000000000
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/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-157-991A-31791

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US-09-264-737-1

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US-09-39-511-1

US-09-39-511-1

US-08-481-476C-3

US-08-48-138-57

US-08-48-138-57

US-08-477-448-57

US-08-477-448-57

US-08-477-488-57

US-08-477-488-57

US-08-48-360-57

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US-08-48-360-57

US-09-136-389-57

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US-09-138-352-5807

US-09-252-991A-28311

US-09-339-511-6

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US-09-356-916-30

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Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 57, Appli
Sequence 57, Appl
Sequence 59, Appli
Sequence 59, Appli
Sequence 59, Appli
Sequence 59, Appli
Sequence 28311, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 30, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 32, Appli
                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                            Sequence 3, Appli
Sequence 31791, A
Sequence 5861, Ap
                                                                                                                                                                                                                                                                              Sequence 3, Application US/09339511

Patent No. 6337385

GENERAL INFORMATION:

APPLICANT: Muir, Tom

APPLICANT: Mo. 6337385ick, Richard P.

APPLICANT: Beavis, Ronald

APPLICANT: Beavis, Ronald

APPLICANT: Ji, Guangyong

TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL

TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL

CURRENT FILING DATE: 1999-06-24

PRIOR APPLICATION NUMBER: US/09/339,511

CURRENT FILING DATE: 1999-06-24

PRIOR FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATENTION OF SEQ ID NOS: 8

ORGANISM: Artificial Sequence

PEATURE:

ORGANISM: Artificial Sequence

PEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

NAME KEY: VARIANT

LOCATION: (5)

OTHER INFORMATION: Xaa represents any amino acid at this position.

US-09-339-511-3
   RESULT 2
US-09-552-991A-31791
US-09-552-991A 31791
Sequence 31791, Application US/09252991A
Patent No. 6551795
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
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US-09-339-511-3
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Best Local S
Matches
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9; Conserv
                                                                                                                                                                                              GVAAXSSLF
                                                                                                                                                                         GVAAXSSLF
                                                                                                                                                                                                                              94.6%; Score 35; DB. larity 100.0%; Pred. No. 2. Conservative 0; Mismatches
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US-08-712-057-8

US-08-712-057-8

US-09-347-878-36

US-09-347-878-36

US-09-356-916-28

US-09-356-916-28

US-09-356-916-28

US-09-252-991A-29161

US-09-252-991A-30503

US-09-339-517-27

US-09-339-517-227

US-09-109-6371A-227

US-09-615-192A-310

US-09-615-192A-310

US-09-422-869-14

US-09-422-869-14
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2.5e+0
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Result No.

Pred. No.

Minimum Maximum

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Total number

Database

Title: Perfect score:

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Scoring table: Sequence:

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US-09-107-532A-5861
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31791
                                                                                                                                                                                          APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY,AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5861:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acids
TYPE: amino acids
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31791
LENGTH: 332
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                             NAME/KEY: misc feature LOCATION: (B) LÖCATION 1...347 SEQUENCE DESCRIPTION: SEQ ID NO: 58
                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 GIAATSMLF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GVAAXSSLF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 100 Beaver Street
                                                                                                                DRGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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66.7%;
 81.1%;
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 Score 30;
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Pred. No. 22;
                                                 5861:
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 DB 4;
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Length 347,
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GENERAL INFORMATION:
APPLICANT: Feng, Paul C.C.
APPLICANT: Feng, Poul C.C.
TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via
TITLE OF INVENTION: Engineering Plant Resistance to Pyridine TITLE OF INVENTION: Expression of Esterase Enzymes
FILE REFERENCE: 38 -21 (10551) RLE3 Pyridine Tolerance
CURRENT APPLICATION NUMBER: US/09/264,737A,
CURRENT FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: 60/077,377
EARLIER APPLICATION NUMBER: 60/077,377
EARLIER APPLICATION WINDER: 1998-03-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fuff, Thomas G.

APPLICANT: Ruff, Thomas G.

TITLE OF INVENTION: Engineering. Plant Resistance to Pyridines via TITLE OF INVENTION: Engineering. Plant Resistance to Pyridines Via TITLE OF INVENTION: Expression of Esterase Enzymes FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance CURRENT APPLICATION NUMBER: US/09/264,737A

CURRENT FILING DATE: 1999-03-09

EARLIER APPLICATION NUMBER: 60/077,377

EARLIER APPLICATION NUMBER: 60/077,377

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PATENTING DATE: 1998-03-10

SUBJECTION: PATENTING DATE: 1998-03-10

SUBJECTION: PATENTING DATE: 1998-03-10

SUBJECTION: PATENTING DATE: 1998-03-10
                                                                                                                                                       ; TYPE: PRT ; ORGANISM: Rabbit US-09-264-737-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Rabbit
US-09-264-737-1
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US-09-264-737-1
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                                                                           Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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249 GVALLSSLF 257
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                                 1 GVAAXSSLF
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7; Conserva
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                                                                         Similarity 7; Conserv
                                                                           Conservative
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                                                                                            81.1%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30; DB Pred. No. 39; 0; Mismatches
                                                                                              Pred. No. 41;
                                                                               Mismatches
                                                                                                               DB 3; Length 566
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                                                                           Gaps
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RESULT 6 US-09-339-511-1

Sequence 1, Application US/09339511

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                                                                                                                                  RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-339-511-1
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0 SEQ ID NO 3 LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08861476C Patent No. 6447786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
                                                                                                 Sequence 59,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/08/861,476C
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE: 63753/7
                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description OTHER INFORMATION: peptide NAME/KEY: VARIANT
                                                                                  tent No.
                                                                                                                                                                                                                                                                                                                               ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (5)
OTHER INFORMATION: Xaa represents any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL ITLE OF INVENTION: INTERFERENCE LE REFERENCE: 600-1-231N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
8; Conserv
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                                                                                                                                                                                   GVNACSSLF
                                                                                                                                                                                                                 GVAAXSSLF
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No. 6337385ick, Richard
Beavis, Ronald
                                                                                                 Application US/07988430
Better, Marc D.
Carroll, Stephen F.
Lane, Julie A.
                                                                                                                                                                                                                                                  Conservative
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                                                Bernhard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guangy
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77.8%;
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88.9%;
                                                Susan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB
Pred. No. 2.5e
0; Mismatches
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2.5e+05;
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2.5e+05;
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                                                                                                                                                                                                                                                            Sequence 5
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                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5416202and, Gret
REGISTRATION NUMBER: 35302
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                           TITLE OF INVENTION: Immunoto:
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                               APPLICANT:
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NITLE OF INVENTION: Materials Comprising and Methods of
NITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (312)
TELEX: 25-3856
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REFERENCE/DOCKET NUMBER:
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STATE: Illinois
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FILING DATE: 19921209
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ADDRESSEE: Bicknell
                                              COUNTRY:
                                                                                                             ADDRESSEE:
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No. 5621083
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                                                                                             6300 Sears Tower,
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                                                                                                                                                                                           Studnika,
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                                                                                                                 Marshall,
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                                                                                                                                                                                               Gary M.
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                                                                                             , O'Toole,
Iower, 233
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                                                                                               Gerstein, Murray &
South Wacker Drive
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US-08-488-113B-57
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APPLICANT: Better, Marc ...
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
APPLICANT: THYENTION: Immunotoxi
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APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION UMMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/ACENT INFORMATION:
ANNEY ACENT INFORMATION:
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                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-UN-1995
CLASSIFICATION: 530
CLASSIFICATION: 530
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LENGTH: 20 amino acids
TYPE: amino acid
                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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TELEFAX: 25-3856
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TLE OF INVENTION:
MBER OF SEQUENCES:
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                                   CATION DATA:
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18-APR-1995
JMBER: US 08/064,691
12-MAY-1993
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Pred. No. 2.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
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PRIOR APPLICATION DATA:
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US 07/988,430
                                                APPLICATION NUMBER: US 00
FILING DATE: 12 MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 09-DEC-1992
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APPLICATION NUMBER: US 08
FILING DATE: 18-APR-1995
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PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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Local Similarity 66:7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JE OF INVENTION: Proteins
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E: Illinois
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500 West Madison
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                                                UMBER: US 07/988,430
09-DEC-1992
MBER: US 07/901,707
19-JUN-1992
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son Street, 34th floor
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Pred. No. 2
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                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/088,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/0-
PRIOR DATE: 10
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08
FILTURE PRIOR NUMBER: US 08
                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FILING DATE: 12-MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ent No.
                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 04-NOV-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/00 FILING DATE: 13-MAY-1996
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LECOMMUNICATION THE
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66.7%;
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                                                            US 07/787,567
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Pred. No. 2.7;
0; Mismatches
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
                                           REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                          REGISTRATION NUMBER:
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Similarity 66.7%;
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                                                                                     MCNicholas, Janet M. RATION NUMBER: 32,918
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500 West Madison Street, 34th floor
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09-DEC-1992
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19-JUN-1992
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Pred. No.
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APPLICATION NUMBER: 08/646,360
FILING DATE: 13.MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12.MAY-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/064,691
FILING DATE: 12.MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxin
TITLE OF INVENTION: Proteins
TITLE OF INVENTION: 173
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 20 amino acids
                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
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LENGTH: 20 amino acids
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APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
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                                                                                                                                        NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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Similarity 66.7%;
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                                                                                : 312/707-8889
312/707-9155
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Pred. No. 2.7;
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US-09-610-838-57
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                 TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08
FILING DATE: 13-MAY-19
APPLICATION NUMBER: PC
FILING DATE: 12-MAY-19
FILING DATE: 12-MAY-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
-610-838-57
                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                         FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: 1
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STATE: Illinois
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UMBER: 08/646,360
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son Street, 34th floor
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Result
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Maximum DB
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Perfect score:
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seq length: 2000000000
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Match
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37
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Maximum Match 100%
Listing first 45 summaries
 GVAAXSSLF 9
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                                                                                                                                      Length
 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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US-10-186-761-9222

US-10-080-170-153

US-10-080-170-538

US-10-080-170-538

US-10-032-950-1

US-09-966-546-10

US-09-966-546-10

US-09-966-546-12

US-09-966-546-12

US-09-965-546-12

US-09-965-546-12

US-09-965-546-12

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US-10-189-940-12

US-10-189-940-12
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                                                                                                                                    Description
      Sequence 3, Appli
Sequence 9222, Ap
Sequence 155, App
Sequence 538, App
Sequence 1, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 12, Appl
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US-10-032-950-3
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10-264-23	09-864-761-4491	-10-032-950-6	-10-032-950-	-10-128-202-	-10-085-198-	-10-128-202-	10-128-202-	-09-949-029-	-10-369-493-409	-10-156-761-106	-10-156-761-980	-10-156-761-	-10-156-761-1317	-10-369-493-908	-09-738-626-525	-10-369-493-1219	-10-369-493-190	-10-369-493-1077	-10-094-749-245	-10-369-493-140	-10-156-761-1243	-10-205-219-6	-09-919-039-3	-10-264-049-38	0-201-444-	9-925-301-14	-10-127-89	US-10-201-444-3
Sequence 1919, Ap Sequence 8741, Ap	quence 44910,	Sequence 6,	equence 5, App	equence 2, App	equence 128, A	equence 8, App	Sequence 7, Appl	equence 6, App	equence 4096,	equence 10602,	equence 9801,	equence 130	equence 13178,	equence 9082,	equence 5251,	equence 12198,	equence 19090,	equence 10775,	equence 2459,	equence 14064,	equence 12438,	equence 67,	ence 343, A	equence 3838	equence 6,	ce 1462, A	nce 57, Ap	` 'D

ALIGNMENTS

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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide; NAME/KEY: VARIANT; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position US-10-032-950-3
                                                                             Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10032950
Publication No. US20020077453A1
GENERAL INFORMATION:
APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453A1ick, Richard P.
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 9
                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                      1 GVAAXSSLF
                                                                               Similarity
9; Conserv
GVAAXSSLF
                                                                             94.6%; Score 35; DB ilarity 100.0%; Pred. No. 7e Conservative 0; Mismatches
                                       9
                                                                                                 DB 13; Length 9; 7e+05;
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Sequence 155. Application US/10080170

Publication No. US20030129601A1

GENERAL INFORMATION:

APPLICANT: COLE, S.T.

ITILE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR

ITILE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR

ITILE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

FILE REFERENCE: 03495.0218

CURRENT APPLICATION NUMBER: US/10/080,170

FURRENT PRILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: 60/270,123

PRIOR FILING DATE: 2001-02-22

NUMBER OF SEQ ID NO 155

SOFTWARE: PASCENTIN Ver. 2.1

SEQ ID NO 155

LENGTH: 163
RESULT 4
US-10-080-170-538
; Sequence 538, Application US/10080170
; Publication No. US20030129601A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                         ; ORGANISM: Mycobacterium leprae
US-10-080-170-155
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Publication No. US20030119018A1
                                                                                                                                                                                                            Matches
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Best Local Similarity
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                                                                                                                          132 GVAAASSAF 140
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77.8%;

    Mismatches

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Pred. No.
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Pred. No. 34;
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22;
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GENERAL INFORMATION:
APPLICANT: Redinbo, Matthew
APPLICANT: Sompp, Bencharit
APPLICANT: Sompp, Bencharit
APPLICANT: Morton, Christopher
APPLICANT: Morton, Christopher
APPLICANT: Morton, Christopher
APPLICANT: Morton, Christopher
APPLICANT: Morton, CRYSTALLIZED MAMMALIAN CARBOXXLESTERASE POLYFEPTIDE AND SCREEN
TITLE OF INVENTION: CRYSTALLIZED MAMMALIAN CARBOXXLESTERASE POLYFEPTIDE AND SCREEN
TITLE OF INVENTION: CRYSTALLIZED MAMMALIAN CARBOXXLESTERASE POLYFEPTIDE AND SCREEN
TITLE OF INVENTION: CRYSTALLIZED MAMMALIAN CARBOXXLESTERASE POLYFEPTIDE AND SCREEN
TITLE OF INVENTION: CRYSTALLIZED MAMMALIAN CARBOXXLESTERASE POLYFEPTIDE AND SCREEN
TURE OF INVENTION: CRYSTALLIZED MAMMALIAN CARBOXXLESTERASE POLYFEPTIDE AND SCREEN
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TURE OF INVENTION: CRYSTALLIZED MAMMALIAN CARBOXXLESTERASE POLYFEPTIDE AND SCREEN
TITLE OF INVENTION: CRYSTALLIZED MAMMALIAN CARBOXXLESTERASE POLYFEPTIDE AND SCREEN
TURE OF INVENTION: CRYSTALLIZED MAMMALIAN CARBOXXLESTERASE POLYFEPTIDE AND SCREEN
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TURE OF INVENTION: CRYSTALLIZED MAMMALIAN CARBOXXLESTERASE POLYFEPTIDE AND SCREEN
TURE OF INVENTION: CRYSTALLIZED MAMMALIAN CARBOXXLESTERASE POLYFEPTIDE AND SCREEN
TURE OF INVENTION CONTROLICATION CARBOXXLESTERASE POLYFEPTIDE AND SCREEN
TURE OF INVENTION
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APPLICANT: COLE, S.T.

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

FILE REFERENCE: 03495.0218

CURRENT APPLICATION NUMBER: U$/10/080,170

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: 60/270,123

PRIOR FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 652

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 538

LENGTH: 167

TYPE: PRT

ORGANION: Mycobacterium tuberculosis
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                                                                       Sequence 1, Application US/10032950
Publication No. US20020077453A1
GENERAL INFORMATION:
APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: Mo. US20020077453A1ick, Richard
APPLICANT: Beavis, Ronald
APPLICANT: Might Guangyong
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Best Local :
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APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES
TITLE OF INVENTION: INTERFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 81.1%; Score 30; DB 12; Local Similarity 77.8%; Pred. No. 1.5e+02; nes 7; Conservative 0; Mismatches 2
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7; Conservat
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                                                                                                                                                                                                                                  RESULT 8
US-09-966-545-10
                                                 Sequence 10, Application US/09966545
Patent No. US30020172999A1
GENERAL INFORMATION:
APPLICANT: Fernances, Elma
APPLICANT: Vernet, Corine
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20020172999A1el Human Proteins and Polynucleotides Encoding
TITLE OF INVENTION: Them
FILE REFERENCE: Cura-46 (15966-546)
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Sequence 10, App...
No. US2002
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Best Local
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Best Local
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CURRENT APPLICATION NUMBER: US/09/9
CURRENT FILING DATE: 2001-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fernandes, Elma APPLICANT: Vernet, Corine APPLICANT: Shimkets, Rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/544,511
PRIOR FILING DATE: 2000-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
CURRENT APPLICATION NUMBER: US/09/966,545
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/544,511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
NAME(KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 160
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LE OF INVENTION: No. US20020168716Alel Human Proteins and Polynucleotides Encoding
LE OF INVENTION: Them
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77.8%;
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Pred. No. 7e+05;
0; Mismatches
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Pred. No. 64;
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-212-10
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LENGTH: 160
TYPE: PRT
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Best Local S
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APPLICANT: Fernandes, Elma
APPLICANT: Vernet, Corine
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20030003462A1el Human Proteins and Polynucleotides Encod
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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                                                                                                                                                                                                                                                                                    Sequence 10, Appropriate Publication No.
APPLICANT: Shenoy, Suresh
APPLICANT: Casman, Stacie
APPLICANT: Rastelli, Luca
TITLE OF INVENTION: No. US20030129613A1el Human
FILE REFERENCE: 15966-546 CIP
CURRENT APPLICATION NUMBER: US/10/189,940
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/303,241
PRIOR FILING DATE: 2001-07-05
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: USSN 60/128,514
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 57
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NUMBER OF SEQ ID NO
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CURRENT APPLICATION NUMBER: US/09/965,212
CURRENT FILING DATE: 2001-09-26
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7; Conserv
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Vernet, Corine
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Anderson, David
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Pred. No.
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                                                                                     Proteins and Polynucleotides Encod
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; ORGANISM: Homo sapiens
US-09-966-546-12
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-940-10
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Best Local S
Matches 7
                                              Sequence 12, Application US/09966545
Patent No. US20020172999A1
GENERAL INFORMATION:
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SEQ ID NO 12
LENGTH: 161
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Best Local
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APPLICANT: Vernet, Corine
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20020168716A1el Human Proteins and Polynucleotides Encoding
TITLE OF INVENTION: Them
              APPLICANT: Fernandes, Elma APPLICANT: Vernet, Corine
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/544,511
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 57
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PRIOR FILING DATE: 2000-03-03
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PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/966,545
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FILING DATE: 2000-04-06
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Richard
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Pred. No.
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Pred. No.
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APPLICANT: Shinkets, Richard A.
APPLICANT: Shinkets, Richard A.
TITLE OF INVENTION: No. US20030003462A1el Human Proteins and Pol)
FILE REFERENCE: Cura-46 (15966-546)
CURRENT APPLICATION NUMBER: US/09/965,212
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US/09/544,511
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 1000-04-06
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 161
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; Publication No. US200
; GENERAL INFORMATION:
APPLICANT: Fernandee
; APPLICANT: Vernet,
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Best Local S
Matches 7
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TITLE REFERENCE: Cura-46 (1.5966-546)
CURRENT APPLICATION NUMBER: US/09/966,545
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/544,511
PRIOR APPLICATION NUMBER: 09/544,511
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Vernet, Corine
APPLICANT: Shimkets, Richa
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ORGANISM: Homo sapiens
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Local Similarity 77.8%;
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Anderson, David
Padigaru, Muralidhara
Casman, Stacie
Rastelli, Luca
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                                                                                                                                             Vernet, Corine
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To. US20030129613A1
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10. US20030003462A1
                              Shenoy, Suresh
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Pred. No.
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Job time : 25.5441 secs

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GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

LENGTH: 1668
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Search completed: January 29, 2004, 15:01:45
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; ORGANISM: Methanobacterium thermoautotrophicum
US-10-369-493-1181
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PRIOR FILING DATE: 2002-04-01
PRIOR FILING DATE: 2002-04-01
PRIOR PELICATION NUMBER: 60/369,065
PRIOR APPLICATION NUMBER: 60/378,730
PRIOR APPLICATION NUMBER: 60/378,730
PRIOR APPLICATION NUMBER: 60/378,730
PRIOR APPLICATION NUMBER: 09/965,212
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/966,545
PRIOR APPLICATION NUMBER: 09/966,546
PRIOR APPLICATION NUMBER: 09/966,546
PRIOR APPLICATION NUMBER: 09/966,546
PRIOR APPLICATION NUMBER: 09/966,545
PRIOR APPLICATION NUMBER: 60/128,514
PRIOR APPLICATION NUMBER: 60/128,514
PRIOR APPLICATION NUMBER: 60/128,514
PRIOR APPLICATION NUMBER: 60/128,592
PRIOR PRICING DATE: 2000-03-03
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SOFTWARE: CUraSeqList version 0.1
SEQ ID NO 12
LENGTH: 161
                                                                                                                                                                                                  Query Match 78.4%; Score 29; DB 12; Length 1668; Best Local Similarity 66.7%; Pred. No. 8.2e+02; Matches 6; Conservative 1; Mismatches 2; Indels
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                                                                                   1273 GIAAISRLF 1281
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Pred. No. 64;
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Listing first 45 summaries
      AVNAXSSLF 9
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Copyright (c) 1993 - 2004 Compugen Ltd
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                                                           S. aureus peptide Cyclic peptide SEQ AgrD-autoinducing Staphylococcus aur Staphylococcus aur Protected peptide
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                                                                                                        24-JUN-1999;
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  (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE
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                                                               98US-0103438
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/label= Unknown
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Peptide mediated q
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S. aureus RN6607 p
Human transport p
Arabidopsis thalia
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S. aureus peptide
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a cyclic peptide derived from the Staphylococcus aureus AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
    Claim
                                                            New
                                                                                                                                                                                                                                    (MUIR/)
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                                       New cyclic peptides, infections
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                                                                        Disclosure;
                                                                                                                                        Muir TW,
                                                                                                                                                       (UYRQ )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                              Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection i
                                                                                                       Novel
                                                                                                                        WPI; 2002-170774/22.
                                                                                                                                                                               24-JUN-1998;
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                                                                                                                                                                                                                                                                                                                              Synthetic
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The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of Staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is a secreted agr-encoded peptide and where the agr locus controls the synthesis of printlence factor and other extracellular proteins responsible for printlence factor and other extracellular peptides may have the sequence NH2-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z residue and COOH other than a thioester

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RESULT 4
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                This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
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AAM50907;

08-MAY-2002

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The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AAM50899-906). The peptide corresponds to the Staphylococcus aureus AgrDII sequence with a Cys5 to Ser mutation (lactorie). It was synthesised on a Wang-resin using an Fmoc N-alpha protection strategy. Following chain assembly, the peptide was cleaved from the support and the Ser-5 residue deprotected by treatment with a trifluoroacetic acid:anisole:water mixture (90:5:5) for 4 hr. The partially protected peptide-alpha carboxylates were then dissolved in DMF and treated with PyBOP and a catalytic amount of dimethylaminopyridine. Cyclization was complete after 2 hr. The remaining protecting groups were then removed by treatment with HF and the peptide by HPIC. The cyclic peptide is capable of inhibiting the agr response of Staphylococcus aureus. The thiololactone structure within native AgrD paptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring can destroy agr response activating activity while preserving and enhancing inhibitory activity. The cyclic peptides are useful for infactorial interference, especially for the treatment of S. aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
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Query Match Best Local Similarity

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DB 23; 9.3e+05;

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Similarity 7; Conserv

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The present sequence is that of a novel synthetic AgrD2 linear thioester peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrB3 containing a beta-lactamase reporter gene fused to the agrB3 containing a beta-lactamase reporter gene fused to the agrB3 containing a beta-lactamase reporter gene fused to the agrB3 containing a beta-lactamase reporter gene fused to the agrB3 containing a beta-lactamase reporter gene fused to the agrB3 containing a beta-lactamase reporter gene fused to the agrB3 containing a beta-lactamase reporter gene fused to the agrB3 containing a beta-lactamase reporter gene fused to the agrB3 containing a beta-lactamase reporter gene fused to the agrB3 containing a beta-lactamase reporter gene fused to the agrB3 containing a beta-lactamase reporter gene fused to the agrB3 containing a beta-lactamase reporter gene fused to the agrB3 containing the analysis of the present peptide was unable to cultured cells at uM concentrations. The invention provides claimed cyclic peptides (see AAMS10899-906 and AAMS1099) cand methods for preparing them. The cyclic peptides are useful for infection
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C and methods for preparing them. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus
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Best Local S
Matches 7
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NEW YORK STATE
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Pred. No. 9.3e+05;
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                                                                                                                     The present sequence is that of a novel synthetic AgrD2 lactone cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactone bond. The peptide is derived from an AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological cativity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrP3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. The lactone AgrD2 peptide inhibited the agr response of group I S. aureus strains without activating the agr response in group I. I or III strains without activating the agr response in group I. I or III especially peptides where the cyclic bond is a lactam or lactone bond. The cyclic peptides are useful for bacterial interference, cespecially for the treatment of S. aureus infection.
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                        subject
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6337385-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgrD2 lactone cyclic peptide
                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-170774/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYRQ ) UNIV ROCKEFELLER. (UYNY ) UNIV NEW YORK STATE
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                       N
                                               7; Conserv
                         VNAXSSLF
VNASSSLF
                                                                                                                                                                                                                                                                                                                                                               Column 9; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     response; inhibitor; antibiotic; antibacterial; therapy; lactone; cyclic.
                                                                                                  9 AA;
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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    peptide"
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  φ
                                                             86.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "note linked to peptide"
                                                 Score 32; DB Pred. No. 9.3e 0; Mismatches
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1;
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AAMS1004 ID AAM

AAM51004 standard; Peptide;

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Query Match
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Thes 7; Conserve
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                                                                                                                                                                                                                                                                                                                   comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of autoinducer-2 agonists or antagonists autoinducer-2 receptor, regulating bacterial also antibiotic compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Synergistic antibiotic compositions
  Staphylococcus aureus infection; cyclic
                          S. aureus peptide #1 used for bacterial interference.
                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 33; 134pp; English
                                                       25-APR-2000
                                                                                AAY67851
                                                                                                        AAY67851 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                           quorum sensing.
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07-DEC-2000; 2000US-254398P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological; vulnerary; pheromone; agr system; accessory gene regulator; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide-mediated quorum sensing inhibitor peptide cyclo-XII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2002
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                                                                                                                                                                         VNASSSLF
                                                                                                                                                                                                    VNAXSSLF 9
                                                                                                                                                                                                                                                                                9 AA;
                                                                                                                                                                                                                             Conservative
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                                                     (first entry)
                                                                                                                                                                                                                                        86.5%;
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                                                                                                                                                                                                                                        Score 32;
Pred. No.
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  peptide; AgrD;
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                                                                                                                                                                                                                                        .3e+05;
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Best Local S
Matches 8
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                                                                                 Misc-difference
                                                                                                                    Staphylococcus aureus
                                                                                                                                          Staphylococcus aureus infection; AgrD; agr response; treatment; virulence factor.
                                                                                                                                                                            Staphylococcus aureus
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                                                                                                                                                                                                                           AAY67861;
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNIV ROCKEFELLER.
UNIV NEW YORK STATE
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                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                             /label= Unknown
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                                                                                             Location/Qualifiers
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Pred. No.
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9.3e+05;
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Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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WPI; 2002-681366/73
                                      Muir TW,
                                                                            (NOVI/)
(BEAV/)
(JIGG/)
                                                                                                                                                                                                 24-JUN-1998;
24-JUN-1999;
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                                                                          ) MUIR T W.
) MAYVILLE P.
) NOVICK R P.
) BEAVIS R.
) JI G.
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8; Conservative
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                                      Mayville P,
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NEW YORK ST
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99US-0339511.
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100.0%; pr
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                                        Beavis
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention. The present invention also describes a method for treating Staphylococcus aureus infection comprising the administration of a composition comprising (I). (I) has antibacterial activity, and can be used as an agr gene response inhibitor. The peptides are useful for treating S. aureus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cyclic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                           Novel synthetic, interference and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM50899 standard; Peptide;
                                                                   Claim 7; Column
                                                                                                                                                                                   WPI; 2002-170774/22.
                                                                                                                                                                                                                                                          (UYRQ ) UNIV
                                                                                                                                                                                                                                                                                                                  24-JUN-1998;
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8; Conserv
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NEW YORK STATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aureus; AgrD; agr response;
infection; therapy; cyclic.
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                                                                                                                           cyclic AgrD-autoinducing peptide for bacterial for treating Staphylococcus aureus infection i
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9.3e+05;
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The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of staphylococcus aureus. It is an AgrD-autoinducing peptide, where

agr response of peptide, where

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RESULT 15
AAM50908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cyclic bond between the Z residue and COOH other than a thioester bond, where X is an amino acid, an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a synthetic or a peptidomimetic or non-amide isostere, Z is a synthetic or a peptidomimetic or non-amide isostere, Z is a synthetic or a biosynthetic anino acid, n is 0-10 and y is 1-10. The cyclic bond is especially a lactam or lactone bond. The thiololactone structure within native AgrD peptides is required for activation of the agr response. Elimination of the thiol ester component of the cyclic ring structure can destroy agr response activating activity while preserving and enhancing inhibitory activity. A claimed method of preparring a cyclic peptide involves: assembling a linear peptide chain on to a solid phase resin support; deprotected peptide with neutral buffer for a time sufficient to form the cyclic peptide and cleave the peptide from the support; and recovering the cyclic peptide. The peptide is useful for another than activity activity and recovering the cyclic peptide. The peptide is useful for another than activity activity as a solid phase resin support; and recovering the cyclic peptide. The peptide is useful for another than activity activity activity.
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus antibacterial;
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                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                             24-JUN-1999;
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(UYRQ ) UNIV ROCKEFELLER
                              24-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           aureus; AgrD; agr response; inhibitor; antibiotic;
infection; therapy; cyclic.
                              98US-090402P
                                                             99US-0339511
                                                                                                                                         9
/note= "note linked to residue 5 to form cyclic
peptide"
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                                                                                                                                                                                                                                                                                    /note= "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                   /label= Dpr(Boc
                                                                                                                                                                                                                                                                                                                                                   note=
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9.3e+05;
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Search comp Job time :

completed: January 29, 2004, 14:52:12 ne : 36.0735 secs

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                                                                                                                                                                                                       Staphylococcus aureus AgrDII sequence with a Cys5 to diaminopropionic cardid (Dpr) mutation (lactam). It was synthesised on a Wang-resin cu using an Fmoc N-alpha protection strategy. Following chain assembly, the peptide was cleaved from the support and the Dpr-5 residue deprotected by treatment with a trifluoroacetic acid.anisole:water carboxylates were then dissolved in DMF and treated with PyBOP. Cyclization was complete after 2 hr. The partially protected peptide-alpha carboxylates were then dissolved in DMF and treated with PyBOP. Cyclization was complete after 2 hr. The remaining protecting groups were removed by treatment with HF and the peptide purified by HPIC. The cyclic peptide is capable of inhibiting the agr response of staphylococcus aureus. The thiololactone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure with a lactam (as in the present case) or a lactone can destroy agr response activating activity while preserving and considered interference, especially for the treatment of S. aureus
                                                                      Query Match
Best Local S
Matches
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AAMS0899-906). The peptide corresponds to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 14; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-170774/22
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                                                                      8; Conserv
                               VNAXSSLF
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                                                                      83.8%; Sillarity 100.0%; I Conservative 0;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                     Score
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1: pir1:*
2: pir2:*
3: pir3:*
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37
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AVNAXSSLF 9
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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A30230
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aminopeptidase (EC
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lysosomal membrane
P2B/LAMP-1 precurs
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adenosyl
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A;Accession: T27215
A;Status: preliminary; translated
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T27215
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 Matches
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ALIGNMENTS

from

GB/EMBL/DDBJ

September

15-Oct-1999 #text_change 31-Jan-2000

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hypothetical protein Y50E8A.m - Caenorhabditis elegans
(;Species: Caenorhabditis elegans
(;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
(;Accession: T31617
R;Steward, C.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z21047
A;Accession: T31617
                                                                               A; Gene: CES
A; Introns:
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
T31617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 4
A;Introns: 70/1; 329/3
C;Superfamily: multidrug resistance protein; ATP-binding cassette
                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;MoLecule type: DNA
A;Residues: 1-2055 <WIL>
A;Cross-references: EMBL:AL117200; NID:e1549770; PIDN:CAB55056.1; CESP:Y50E8A.m
A;Experimental source: clone Y50E8A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z99281; PIDN:CAB16503.1; GSPDB:GN00022; A;Experimental source: clone Y57G11C C;Genetics:
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A;Residues: 1-633 <WIL>
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Best Local S
Matches 7
                       Query Match
Best Local :
Local Similarity nes 7; Conserv
                                                                               CESP:Y50E8A.m
ns: 273/3; 447/1;
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7; Conserv
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                                                                                 526/1; 735/1; 1247/1; 1418/1; 1494/1; 1753/3
    86.5%; Score 32; DB 77.8%; Pred. No. 44; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.9%; Score 34; DB 2; 77.8%; Pred. No. 3.9; ive 1; Mismatches
                                         BG
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                                         Length 2055;
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RESULT 5
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A;Authors: Yoo, H.; Tao, Y.; Biddl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n-carbamoyl-beta-alanine amidohydrolase PA0444 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002 C;Accession: G98348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-carbamoyl-beta-alanine amidohydrolase [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A,Reference number: A97359; MUID:21608551; PMID:11743194
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                                                                                                                                                                                                                                        ;Map position:
;Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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                                                                                                                                                                                                                                                                              Gene: AGR_L_3478
                                                                                                                                                                                                                                                                                                                 Cross-references: GB:AE007870; PIDN:AAK90313.1;
                                                                                                                                                                                                                                                                                                                                     Molecule type: DNA
Residues: 1-441 <KUR>
                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: AH2933
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77.8%;
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77.8%;
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Pred. No.
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kelz, B.;
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N;Alternate names: protein YIL109c
C:Species: Saccharomyces cerevisiac
C;Date: 02-Dar-'^^^
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A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aure A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: C89995
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                                                                                               R;Viret, J.F.; Schantz, M.L.; Schantz, R. Nucleic, Acids Res. 18, 7179, 1990
A;Title: Nucleotide sequence of a maize cDNA coding for A;Reference number: S13098; MUID:91088340; PMID:2263499
A;Accession: S13098
                                                                                                                                                                                                chlorophyll a/b-binding protein precursor - maize C;Species: Zea mays (maize) C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 C;Accession: S13098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AgrD protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
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A;Map position: 9L
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A;Cross-references: EMBL:X55892; NID:g22354; PIDN:CAA39376.1; C;Superfamily: chlorophyll a/b-binding protein
                                                                                                                                                                                                                                                                                 S13098
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A;Experimental source:
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A; Residues: 1-47 < KUR>
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C;Genetics:
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A; Residues: 1-926 <BOW>
                                        A; Molecule type: mRNA
A; Residues: 1-265 < VIR>
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                                                                                A;Status: preliminary
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Best Local S
Matches 7
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Pred. No.
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                         PID: g22355
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, Y.Y.; Lin, S.X; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nypothetical protein T5Al4.12 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: A96597
                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T30942
R;Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughey, W.H.; Dowdy, A.K.
submitted to the EMBL Data Library, November 1997
A;Description: Molecular comparison of aminopeptidase cDNAs and gene structure between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aminopeptidase (EC 3.4.11.-) - Indian meal moth
C;Species: Plodia interpunctella (Indian meal moth)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 01-Feb-2002
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A;Cross-references: EMBL:AF034483; NID:g2645992;
C;Superfamily: membrane alanyl aminopeptidase
                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z20942
A; Accession: T30942
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A;Residues: 1-315 <STO>
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                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
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                                                                                                                                                                                                       Keywords: aminopeptidase
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77.8%;
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Pred. No. 62;
2; Mismatches
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0; Mismatches
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; Dewar, K.,
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A;Description: Sulfolobus solfatarious complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-1016 <ZHU>
A;Residues: 1-1016 <ZHU>
A;Cross-references: EMBL:AF034484; NID:g2645994; PID:g2645995; PIDN:AAC36147.1
C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T30943

R;Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughey, W.H.; Dowdy, A.K. submitted to the EMBL Data Library, November 1997

submitted to the EMBL Data Library of sminneridase cDNAs and gen
A;Molecule type: mRNA
A;Residues: 1-382 <CHS>
A;Cross-references: GB:J03881; NID:g198706; PIDN:AAA39411.1; PID:g293692
A;Note: the authors translated the codon ATT for residue 1 as Leu and CCG
C;Superfamily: lysosome-associated membrane protein
                                                                                                              C;Accession: A28067
R;Chen, J.W.; Cha, Y.; Yuksel, K.U.; Gracy, R.W.; August, J.T.
J. Biol. Chem. 263, 8754-8758, 1988
J. Biol. Chem. 263, 8754-8758, 1988
A;Title: Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycopx:
A;Reference number: A28067; MUID:88243732; PMID:3379044
A;Accession: A28067
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A28067
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C;Species: Plodia interpunctella (Indian meal moth)
C;Date: 19-May_2000 #sequence_revision 19-May-2000
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A; Residues: 1-271 <KUR>
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A;Accession: F90350
                                                                                                                                                                                                                                           lysosomal membrane glycoprotein LAMP-1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change
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6; Conservation
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Pred. No. 25;
2; Mismatches
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Pred. No. 62;
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24-May-2001

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G.; Awayez, M.J.; Cha hi-Ngoc, H.P.; Redder

20-Aug-1999

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Gaps

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A;Title: Isolation and sequencing of a cDNA clone encoding 107 kDa sialog A;Reference number: $03331; MUID:89153580; PMID:2920835 A;Accession: $03331 and part of type: mRNA A;Residues: 22-407 <HIM> A;Residues: 22-407 <HIM> A;Residues: 22-407 cHIM> A;Cross-references: EMBL:X14765; NID:g56577; PIDN:CAA32873.1; PID:g56578 A;Note: part of this sequence, including the amino end of the mature prot C;Superfamily: lysosome-associated membrane protein C;Keywords: glycoprotein; membrane protein C;Keywords: glycoprotein; membrane glycoprotein, 107K #status experimen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: sialoglycoprotein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Oct-1989 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
C;Accession: A30200; S03331
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 03-May-1996
C;Accession: A60534
R;Heffernan, M.; Yousefi, S.; Dennis, J.W.
Cancer Res. 49, 6077-6084, 1989
A;Title: Molecular characterization of P2B/LAMP-1, a major protein target of a metastasi
A;Reference number: A60534; MUID:90002989; PMID:2676155
                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-407 kHOW>
A; Cross-references: EMBL:J03672
A; Note: the authors translated the codon GGG for residue 15 as
R; Himeno, M.; Noguchi, Y.; Sasaki, H.; Tanaka, Y.; Furuno, K.;
FEBS Lett. 244, 351-356, 1989
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A;Molecule type: mRNA
A;Residues: 1-405 <HEF>
C;Superfamily: lysosome-associated membrane protein
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C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 03-May-1996
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Matches 6
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Best Local S
Matches 6
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Accession: A30200
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                                                                                                                       Query Match
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les 6; Conserv
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: Derived protein sequence, oligosaccharides, and membrane insertion of
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282 MNATSSLF 289
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1; Mismatches
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Pred. No.
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Search completed: January 29, Job time : 12.1176 secs

2004, 14:58:22

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A;Cross-references: GB:M31939; GB:J03356; NID:g153210; PIDN:AAA26719.1; FA;Note: the authors translated the initiation codon GTG for residue 1 as R;HOTII, M.; Ishizaki, T.; Paik, S.Y.; Manome, T.; Murooka, Y. J. Bacteriol. 172, 3644-3653, 1990

A;Title: An operon containing the genes for cholesterol oxidase and a cythic accession: S15809; MUID:90299781; PMID:2361941

A;Accession: S15810
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                                                                                                                                                                                                      C;Keywords: oxidoreductase
F;1-42/Domain: signal sequence #status predicted <SIG>
F;43-546/Product: cholesterol oxidase #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:M31939; GB:J03356; NID:g153210
R;Purcell, J.P.; Greenplate, J.T.; Jennings, M.G.; Ryerse, J.S.; Pershing, J.C.; Sims Biochem. Biophys. Res. Commun. 196, 1406-1413, 1993
A;Title: Cholesterol oxidase: a potent insecticidal protein active against boll weevi A;Reference number: PC2002; MUID:94071904; PMID:8250897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Nucleotide sequence of the gene for cholesterol A;Reference number: A32260; MUID:89123081; PMID:2914858 A;Accession: A32260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Streptomyces sp.
C;Date: 20-Oct-1989 #sequence revision 20-Oct-2000 #text_change 20-Oct-2000 C;Accession: A32260; S18810; FC2002
R;Ishizaki, T.; Hirayama, N.; Shinkawa, H.; Nimi, O.; Murooka, Y.
                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 'XXXTF',48-54,'XX',57,'X',59-60 <PUR>
                                                                                                                                                                                                                                                                                                                                                                                      A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-30 < HOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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mus musculu saccharomyc oenothera h avian infec

drosophila avian

| murine coro | ancylobacte | haemophilus

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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PLEC_CAUCR
AWPE_HUMAN
TSH_DROME
TAGB_DICDI
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CB29_MAIZE
PROB_STRTR
1A1D_PSEFL
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SC24_YEAST
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01-FEB-1995 (Rel. 31, Created)

01-FEB-1995 (Rel. 31, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

Protein transport protein Sec24 (Abnormal nuclear mor.

SEC24 OR ANUI OR YIL109C.

Saccharomyces cerevisiae (Baker's yeast).

Saccharomyces (Baker's yeast).

Saccharomycetales; Saccharomycetanes; Saccharomyces.
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PubMed=9169870;

Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,

Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,

Chillingworth T., Hunt S., Jagels K., Jones M., Lye G.,

Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,

Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";

Nature 387:84-87(1997).
     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                    "Sec24p and Issip function interchangeably formation from the endoplasmic reticulum in cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20219212; PubMed=10753972; Feng R., De Antoni A., Gallwitz D.; "Bvidence for overlapping and distinct fu of coat protein Sec24p family members."; J. Biol. Chem. 275:11521-11528(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
MEDLINE=20177547; PubMed=10712514;
Kurihara T., Hamamoto S., Gimeno R.E.,
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                                                                                                                                                                          BIOI. Cell 11:983-998 (2000).

BIOI. Cell 11:983-998 (2000).

FUNCTION: COMPONENT OF THE COPIT COAT, THAT COVERS ER-DERIVED FUNCTION: COMPONENT OF THE COPIT END THE ENDOPLASMIC RETICULUM TO THE GOLGI APPARATUS. COPII ACTS IN THE CYTOPLASM TO PROMOTE THE TRANSPORT OF SECRETORY, PLASMA MEMBRANE, AND VACUOLAR PROTEINS FROM THE ENDOPLASMIC RETICULUM TO THE GOLGI COMPLEX.

SUBUNIT: COPII IS COMPOSED OF AT LEAST FIVE PROTEINS: THE SEC23/24 COMPLEX, THE SEC13/31 COMPLEX AND SAIL (By Similarity).

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: BELONGS TO THE SEC23/SEC24 FAMILY. SEC24 SUBFAMILY.
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AF10_MOUSE
PDRC_YEAST
YCT1_OENHO
RRPB_IBVB
RRPA_CVMJH
GVPA_ANCAQ
Y228_HAEIN
ATPE_CHAGI
LGB1_VICPA
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COMD_METJA
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Minimum Maximum

DB seq

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Post-processing:

Scoring table:

Title: Perfect score:

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protein

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RESULT
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"Nucleotide sequence of a maize cDNA coding for a light-harvesting rehlorophyll ab binding protein of photosystem II.";

L Nucleic Acids Res. 18:719-7179(1990).

C -!- FUNCTION: THE LIGHT-HARVESTING COMPLEX (LHC) FUNCTIONS AS A LIGHT RECEPTOR, IT CAPTURES & DELIVERS EXCITATION ENERGY TO PHOTOSYSTEMS WITH WHICH IT IS CLOSELY ASSOCIATED. THE N-TERMINUS OF THE PROTEIN CETTENUS INTO THE STROMA WHERE IT IS INVOLVED WITH ADHESION OF EXTENUS INTO THE STROMA WHERE IT IS INVOLVED WITH ADHESION OF CORANAL MEMBRANES AND PHOTOREGULATED BY REVERSIBLE PHOSPHORYLATION OF ITS THREONINE RESIDUES; BOTH ARE BELLEVED TO MEDIATE THE DISTRIBUTION OF EXCITATION ENERGY BETWEEN PHOTOSYSTEMS I AND INSTRUMENTIAL A-B BINDING PROTEINS.

C -!- SUBUNIT: THE LHC COMPLEX CONSISTS OF CHLOROPHYLLS (A & B) AND CHLOROPHYLL A-B BINDING PROTEINS.
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Pfam;
                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAIZE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4577;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays (Maize).
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S0001371; SEC24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S48463;
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PR04815; Sec23 helical; 1
PP04811; Sec23 retunk; 1
PP04810; zf-Sec23 Sec24; 1.
PP04810; zf-Sec23 Sec24; 1.
port; Protein transport; Golgi stack; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VNAXSSLF 9
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110
157
926 AA;
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(Rel. 23, Last sequence update)
(Rel. 41, Last annotation update)
A-B binding protein M9, chloroplast precursor
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103635 MW;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>--</u>
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1; 35E2BDD24CC75899 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Best Local S
Matches 7
EMBL; X92418; CAA63147.1; -.
HAMAP, MF 00456; -; 1.
InterPro; IPR001048; Aa kinase.
InterPro; IPR001057; Glu Skinase.
Pfam; PF00696; aakinase; 1.
PRINTS; PR00474; GLUSKINASE.
PROSTIE; P800902; GLUTAMATE_5 KINASE; 1.
Transferase; Kinase; Proline Biosynthesis.
SEQUENCE 267 AA; 28966 MW; B7244BC2B7432BE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM TRANSMEM
                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                      of the proBA operon and its products.";
Microbiology 142:3275-3282(1996)
-!- FUNCTION; Catalyzes the transfer of a phosphate group to glutamate
to form glutamate 5-phosphate which rapidly cyclizes to 5-
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-AFCC 19258;
MEDLINE=97124211; PubMed=8969524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlorophyll; Photosynthesis; Photosystem I Thylakoid; Membrane; Chloroplast; Transit
                                                                                                                                                                                                                                                                                 oxoproline.
-!- CATALYTIC ACTIVITY: ATP + L-glutamate =
                                                                                                                                                                                                                                                                                                                                                           Limauro D., Falciatore A., Basso A.L., "Proline biosynthesis in Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glutamate 5-kinase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P96488;
30-MAY-2000
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InterPro; IPR00
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                                                                                                                                                                                                                             PATHWAY: Proline biosynthesis; first step.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the glutamate 5-kinase family.
                                                                                                                                                                                                                                                          phosphate.
PATHWAY: F
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(Rel. 39,
(Rel. 41,
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32
99
151
219
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77.8%;
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Last annotation update)
C 2.7.2.11) (Gamma-glutamyl kinase)
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Pred. No. 7.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267
                                                                                                                                          (See http://www.isb-sib
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcaceae
                                                                                                                                                                 There are no restrictiong as its content is
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                                                                                                                                                                                                                                                                                  + L-glutamate
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              protein 1.";

J. Biol. Chem. 265:7419-7423(1990).

-I- FUNCTION: PRESENTS CARBOHYDRATE LIGANDS

IMPLICATED IN TUMOR CELL METASTASIS.

-I- SUBCELLULAR LOCATION: Type I membrane protein SHUTTLES BETWEEN LYSOSOMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JLT 4
LMOUSE
LMP1 MOUSE
P11438; Q62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 25-406 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=88243732; PubMed=3379044;
Chen J.W., Cha Y., Yuksel K.U., Gracy R.W., August J.T.;
"Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycoprotein mouse LAMP-1. Sequence similarity to proteins bearing onco-differentiation antigens.",
Onco-differentiation antigens.",
J., Biol. Chem. 263:8754-8758(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization and cloning of lgp110, glycoprotein from mouse and rat cells."; J. Biol. Chem. 265:12036-12043(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE PROM N.A.
MEDLINE 90307738; PubMed=2142158;
MEDLINE 90307738; SubMed=2142158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1989 (Rel. 12, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (LGP-A)
(LGP-120) (CD107A) (P2B).
EMBL; M32015; AAA39428.1; --
EMBL; M25244; AAA39869.1; --
EMBL; J03881; AAA39411.1; --
PIR; A28067; A28067.
PIR; A60534; A60534.
                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90237040; PubMed=2332434; Arterburn L.M., Earles B.J., August J.T.; "The disulfide structure of mouse lysosome-associated membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heffernan M., Yousef:
Submitted (FEB-1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Granger B.L., Green S. Helenius A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBRANE
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Yousefi
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Rodentia;
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he EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Type I membrane protein. Lysosomal. BETWEEN LYSOSOMES, ENDOSOMES, AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred
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1914562; P97620;

01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (LAMP Lysosomal membrane glycoprotein)

kDa lysosomal membrane glycoprotein) (LGP-120) (CD107A).

LAMP1 OR LAMP-1.
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"Derived protein sequence, of the 120-kDa lysosomal m
                     SEQUENCE FROM N.A. MEDLINE=89017240; I Howe C.L., Granger
                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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PROSITE; PS00311; LAMP_2; 1.
Transmembrane; Glycoprotein;
SIGNAL 1 24
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Pfam; PF01299; Lamp; 1.
PRINTS; PR00336; LYSASSOCTDMP
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EMBL; X14765; CAA32873.1; -.
EMBL; U75406; AAB19108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=89153580; PubMed=2920835;
Himeno M., Noguchi Y., Sasaki H.,
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SIGNAL
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PROSITE; PS00310; LAMP 1; 2.
PROSITE; PS00311; LAMP 2; 1.
Transmembrane; Glycoprotein; Lysosome; Signal.
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InterPro; IPR002000; Lamp.
Pfam; PF01299; Lamp; 1.
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PDB; 188S; 09-FEB-99.

PDB; 1CBC; 10-MAR-99.

PDB; 1CC2: 11-MAR-99.

PDB; 1CT2: 11-MAR-99.

PDB; 1MXT; 25-FEB-03.

PDB; 1MXT; 25-FEB-03.

InterPro; IPR000172; GMC oxred.

InterPro; IPR006311; Tat-

Pfam, PP05199; GMC_oxred_C; 1.

TIGREAMS, TIGR01409; TAT signal seq; 1.

PROSITE; PS00623; GMC_OXRED_1; 1.

PROSITE; PS00624; GMC_OXRED_2; FALSE_NEG.
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Cholesterol
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-!- COFACTOR: FAD.
-!- PATHWAY: CHOLESTEROL METABOLISM
-!- SUBUNIT: Monomer.
-!- SUBUNIT: Monomer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces sp.";
J. Bacteriol. 171:596-601(1989).
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                                                                                                                                                                      EMBL; M31939; AAA26719.1; -. PIR; A32260; A32260.
                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 38:4277-4286(1999).
-!- CATALYTIC ACTIVITY: Cholesterol + O(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Crystal structure determination of cholesterol Streptomyces and structural characterization of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishizaki T., Hirayama N., Shinkawa H., Nimi O., U
"Nucleotide sequence of the gene for cholesterol
Streptomyces sp.";
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SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.
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(Rel. 42, Last annotation update)
oxidase precursor (EC 1.1.3.6) (CHOD)
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GV -> EF (IN REF. 3).
N -> T (IN REF. 3).
SD -> VT (IN REF. 3).
SD -> VT (IN REF. 3).
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Flavoprotein; FAD; 3D-structure
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Q59189;
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15-DEC-1998 (Rel. 37, Last seque)
16-OCT-2001 (Rel. 40, Last anno
1 16-OCT-2001 (Rel
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STRAINARTCC 35210 / B31;

MEDLINE=98065943; PubMed=9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,

Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn

Doughetty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M

van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,

Utterback T., Watthey L., McDonald L., Arriach P., Bowman C.,

Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,

"Genonic sequence of a Lyme disease spirochaete, Borrelia

"Genonic sequence of a Lyme disease spirochaete, Borrelia
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                                                                                      Ojaimi C., Davidson B.E., Saint-Girons I., Old I.G.;

"Conservation of gene arrangement and an unusual organization of genes in the linear chromosomes of the Lyme disease spirochaetes Borrelia burgdorferi, B. garinii and B. afzelii.;

microbiology 140:2931-2940(1994).

"IT PUNCTION: TOPOISOMERASE IV IS ESSENTIAL FOR CHROMOSOME SEGREGATION. IT HAS RELAXATION OF SUPERCOILED DNA ACTIVITY.

PERFORMS THE DECATEMATION EVENTS REQUIRED DURING THE REPLICAT PERFORMS THE DECATEMATION EVENTS REQUIRED DURING THE REPLICAT OF A CIRCULAR DNA MOLECULE (BY SIMILARITY).

"I- SUBUNIT: COMPOSED OF TWO SUBUNITS: PARC AND PARE."

"I- SIMILARITY: Belongs to the type II topoisomerase family."
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-83 FROM N.A.
STRAIN=212;
MEDLINB=95111614; PubMed=7812434;
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PARE OR BB0036.
Borrelia burgdorfari (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
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K., Gwinn M
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RESULT 8

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01-OCT-1989 (Rel. 12, Last sequence
15-SEP-2003 (Rel. 42, Last annotatic
3-hydroxy-3-methylglutaryl-coenzyme
CoA reductase 1).
HMG1 OR YML075C.
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InterPro; IPR001241; DNA_topoisoII.
Ffam; PF08204; DNA_gyraseB; 1.
Pfam; PF08204; DNA_GyraseB; 1.
Pfam; PF08218; HATPase c; 1.
PRINTS; PR00418; TP127AMILY.
SMART; SM00387; HATPase c; 1.
SMART; SM00387; TOPCI; 1.
SMART; SM00337; TOPCISOMERASE II; 1.
PROSITE; P800177; TOPCISOMERASE II; 1.
ISOMERASE; Topoisomerase; ATP-bInding; Complete proteome.
SEQUENCE 599 AA; 68774 MW; B5901F17B1CC7721 CRC64;
                          SEQUENCE OF 776-965 FROM N.A.

MEDILINE=86287298; PubMed=3526336;

Basson M.E., Thorsness M., Rine J.;

Basson M.E., Thorsness M., Rine J.;

"Saccharomyces cerevisiae contains two functional genes encoding hydroxy-3-methylglutaryl-coenzyme A reductase.";

Proc. Natl. Acad. Sci. U.S.A. 83:5563-5567(1986).

-!- FUNCTION: THIS TRANSMEMBRAME GLYCOPROTEIN IS INVOLVED IN THE CONTROL OF CHOLESTEROL BIOSYNTHESIS. IT IS THE RATE-LIMITING ENZYME OF THE STEROL BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89127221; PubMed=3065625;
Basson M.E., Thorsness M., Finer-Moore J., Stroud
"Structural and functional conservation between ye
hydroxy--methylglutaryl coenzyme A reductases, the
enzyme of sterol biosynthesis.";
mol. Cell. Biol. 8:3797-3808(1988).
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PIR; D70104; D70104.
HSSP; P06982; 1AJ6.
TIGR; BB0036; -.
                                                                                                                                                                                                                                                                          Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitchead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacci
Saccharomycetales; Saccharomycetaceae; Saccharomyces
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[3]
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01-CCT-1996 (Rel.
Hypothetical 57.
YJR122W OR J2043.
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GO; GO:0005789; C:endoplasmic reticul GO; GO:0005635; C:nuclear membrane; Interpro; IPR002202; HMG-COA red.
Interpro; IPR004554; HMG-COA_R-NADP.
Interpro; IPR004754; HMG-COA_R-NADP.
Interpro; IPR000731; SSD_5TM.
Pfam; PF00368; HMG-COA_R-GG; IPR000731; SSD_STM.
Pfam; PF00368; HMG-COA_R-GG; IPR000731; IPR0000731; IPR0000731; IPR0000731; IPR0000731; IPR0000731; IPR0000731; IPR0000731; IPR0000731; IP
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PROSITE; PS00066; HMG_COA_REDUCTASE 1;
PROSITE; PS00318; HMG_COA_REDUCTASE 2;
PROSITE; PS01192; HMG_COA_REDUCTASE 3;
PROSITE; PS50065; HMG_COA_REDUCTASE 4;
PROSITE; PS50156; SSD; 1.
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EMBL; Z46373; CAA86503.1; -.
PIR; A30239; A30239.
SGD; S0004540; HMG1.
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-!- SIMILARITY: BELONGS TO THE HMG-COA REDUCTASE FAMILY
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hydroxy-3-methylglutaryl-CoA+ 2 NADPH.
-i- PATHWAY: Cholesterol biosynthesis.
-i- SUBCELLULAR LOCATION: Integral membrane
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(See http://www.isb-sib.ch/announce/
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PIR; S57145; S57145.
TRANSPAC; T03226; -
SGD; S0003883; CAF17.
InterPro; IPR006222; GCV_T.
Pfam; PF01571; GCV_T; 1.
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DNA polymerase III alpha s
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-NCTC 11168;

MEDLINE=20150912; PubMed=10688204;

MEDLINE=20150912; PubMed=10688204;

Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,

Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

Whitehead S., Barrell B.G.;

Whitehead S., Barrell B.G.;

Whe genome sequence of the food-borne pathogen Campylobacter jejuni

reveals hypervariable sequences.";

Nature 403:655-668(2000).

III IS A COMPLEX, MULTICHAIN ENZYME

TENTONICIES DOR MOGT OF THE BEBLICATIVE SYNTHESIS IN BACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DP3A CAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campylobacter jejuni.
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Campylobacteraceae, Campylobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical SEQUENCE 49
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SUBURNIT: INA polymerase III contains a core (composed of alpha, epsilon and theta chains) that associates with a tau subunit. To core dimerizes to form the POLIII' complex. PolIII' associates with the gamma complex (composed of gamma, delta, delta', psi a chi chains) and with the beta chain to form the complete DNA polymerase III complex (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                      FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA. THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY. THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY). CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
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InterPro; IPR003141; PHP N.
InterPro; IPR003141; PHP N.
InterPro; IPR004805; PolC_alpha.
Pfam; PF02811; PHP_C; 1.
Pfam; PF02281; PHP_N; 1.
SMART; SM00481; POLILIAC; 1.
TIGREAMS; TIGR00594; PolC; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                               Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyaji Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanob; synechocystis sp. strain PCC5803. I. Sequence features in tregion from map positions 64% to 92% of the genome."; DNA Res. 2:153-166(1995).

11. COCATION: Binds I zinc ion per subunit (By similarity).
12. SUBCELLULAR LOCATION: Integral membrane protein (Potent SINILARITY: BELONGS TO PEPTIDASE FAMILY M50B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an
                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-scr send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Cyanobacteria; Chroococcales; Synechocystis. NCBI_TaxID=1148;
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Q55518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                            EMBL; D64006; BAA10876.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96127529;
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| protein sll0528 (EC 3.4.24.-).
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InterPro; IPR000644; InterPro; IPR001193; InterPro; IPR006025; PIR; S76029; S76

CBS_domain.
Peptidase_M50.
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30-MAY-2000
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Pfam; PFO
SMART; SM
PROSITE;
HSSP; P08859; IGLC.

HAMAP, MF 00186; -; 1.
InterPro; IPR000577; FGGY_kin.
InterPro; IPR005999; Glycerol_kin.
Pfam; PF00370; FGGY_C; 1.
Pfam; PF02782; FGGY_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98196666; PubMed=9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus.";
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Bacteria; Aquificae;
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Repeat; CBS domain; Cc
                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: KEY ENZYME IN THE REGULATION OF GLYCEROL UPTAKE AND METABOLISM.
-!- CATALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate
-!- PATHWAY: Glycerol utilization; rate-limiting step.
-!- PATHWAY: GLYCEROK TO THE FUNCTIONSE / GLUCONOKINASE /
GLYCEROKINASE / XYLULOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLPK OR AQ 434.
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PF02163; Peptidase_MSO;
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lase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brown S., Cronin R., Chillingworth T., Churcher C.M.,
RA Brown S., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle D.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Cliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Kelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonpyez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Muller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Muller-Auer S.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
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Hypothetical protein C3A12.15 in chrom
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PROSITE; PS00445; FGGY_KNASES 2;
PROSITE; PS00933; FGGY_KNASES 1;
Glycerol metabolism; Transferase; I
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is no modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WEDLINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A.,
                                      EMBL; Z95395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHPO
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                                         CAB08743.1;
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55297 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.0%;
75.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (PROBABLE).
; CE95F0E8FF593B37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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1.
Kinase; ATP-binding
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RESULT NAME OF THE RAA A MERCHANA MERCHANA A MERCHANA A MERCHANA A MERCHANA A MERCHANA A MERCHANA A MERCHANA A
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Howkins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Kicharde S., Ashburner M., Henderson S.N.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Baltek R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Bavenport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Bavenport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Bavenport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Bavenport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Bavenport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Bavenport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Bavenport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Glodek A.J., Evantellan A.E., Garg N.S., Gelbart W.M., Glasser X.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kalp D., Lai Z.,
RA Melson D.R., Naicha N.J., McLeod M.P., McPherson D.L.,
RA Melson D.R., Naicha N.J., McLeod M.P., McPherson D.L.,
RA Melson D.R., Naicha N.J., McLeod M.P., McPherson D.L.,
RA Melson D.R., Naicha N.J., McLeod M.P., McMang X.,
RA Melson D.R., Naicha N., Strong R., Sunth T.,
RA Welson D.R., Naicha N., Strong R., Sunth T.,
RA Welson D.R., Naicha N., Strong R., Sunth T.,
RA Welson D.R., Naicha N., Strong R., Sunth T.,
RA Welson N., Woodar
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16-OCT-2001
28-FEB-2003
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MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative glutamine-dependent NAD(+) synthetase (EC synthase [glutamine-hydrolyzing]). CG9940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
SEQUENCE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GeneDB_SPombe; SPAC3A12.15; Pfam; PF04100; Vps53_N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DROME
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756 AA; f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366
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Pred. No. 1.2e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Best Local S
Matches
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F1yBase; EBgn0030512; CG9940.
InterPro; IPR0030594; NAD synthase.
InterPro; IPR003010; NtlSe/CNhydtse.
pfam; PF00795; CN_hydrolase; 1.
Pfam; PF002404; NAD synthase; 1.
Pfam; PF002540; NAD synthase; 1.
TIGRPAMS; TIGR00557; nadE; 1.
PROSITE; PS50265; CN_HYDROLASE; 1.
PROSITE; PS50265; CN_HYDROLASE; 1.
PROSITE; PS50265; CN_HYDROLASE; 1.
PROMAIN
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SOMAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UL-OCT-1994 (Rel. 30, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Non-motile and phage-resistance protein (EC 2.7.3.-).
PLEC OR CC2482.
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P37894;
01-OCT-1994
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Nierman W.C., Feidblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.C., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus.", proc. Matl. Acad. Sci. U.S.A. 98:41341(2001).

1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM INVOLVED IN THE REGULATION OF POLAR ORGANELLE DEVELOPMENT. PLEC PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 19089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 19089 / CB15;

WEDLINE=93133840; PubMed=8421698;

Wang S.P., Sharma P.L., Schoenlein P.V., Ely B.;

"A histidine protein kinase is involved in polar development in Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 90:630-634 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caulobacter crescentus.
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
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-!- SIMILARITY: IN THE C-TERMINAL SECTION, BELC

-SYNTHETASE PARILY.

-!- SIMILARITY: Contains 1 CN hydrolase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
STRAIN=ATCC 19089
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21173698;
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787 L
362 A
357 B
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Pred. No. 1.3e+02;
1; Mismatches 2;
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Matches 6
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InterPro; IPR00458; Bact sens pr C.
InterPro; IPR003661; His kinh.
InterPro; IPR005667; His kinhse.
InterPro; IPR00514; PAS domain.
Pfam; PF00512; Hiska; I.;
Pfam; PF00512; Hiska; I.;
Pfam; PF00989; PAS; 2.
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                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00387; HATTRASE C; 1.
SMART; SM00388; HISKA; 1.
SMART; SM00091; PAS; 2.
TIGREPAMS; TIGR00229; SENSOTY box; 2.
PROSITE; PS50109; HIS KIN; 1.
PROSITE; PS50109; HIS KIN; 1.
PROSITE; PS50112; PAS; 1.
SENSOTY transduction; Transferase; Kinase; Transmembrane;
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EMBL; AE005917; AAX24453.1; --.
PIR; AE7557; AB7557.
PIR; S27533; S27533.
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PHOSPHATE TO A RESPONSE REGULATOR.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- PTM: THE C-TERMINAL IS CAPABLE OF AUTOPHOSPHORYLATION.
-!- SIMILARITY: Contains 1 histidine kinase domain.
-!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

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Q9u275 caenorhabdi
Q8u275 caenorhabdi
Q8u275 caenorhabdi
Q8u266 streptomyce
Q32546 streptylococ
Q92214 coppinus cativ
Q91kk3 oryza sativ
Q92vu6 arabidopsis
Q94bs2 arabidopsis
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Q95780 arabidopsis
Q95780 arabidopsis
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Y57G11C 1
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ALIGNMENTS

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investigating biology.";
Science 282:2012-2018(1998).
Science 282:2012-2018(1998).
-- SIMILARITY: BELONGS TO THE ABC TRANEMBL; Z99281; CAB16503.1; ...
EMBL; Z99281; CAB16503.1; ...
WormPep; Y57G110.1; CE14926.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003140; ABC_TMICRASporter.
InterPro; IPR003439; ABC_Transporter.
                                                                    Pfam; PF00664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transporter
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER
ATP-binding; Transport; ABC_TRANSPORTER
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
MCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MCMUTTAY A.A.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans: A platform for
                                                   71699 MW; 8807414AA9884058 CRC64;
     91.9%;
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Q9U275;
01-MAY-2000 (TrEMBL:
01-MAY-2000 (TrEMBL:
01-MAR-2003 (TrEMBL:
Y50E8A.16 protein.
                                                                             Q8UBE6 PRELIMINARY; PRT; 441 AA.

Q8UBE5;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
N-carbamoyl-beta-alanine amidohydrolase.
NAB OR ATU3070 OR AGR L. 3478.

AVAB OR ATU3070 OR AGR L. 3478.

Bacteria; Procebbacteria; Alphaproteobacteria; Rhizonatoria procebbacteria; Alphaproteobacteria; Rhizonatoria procebbacteria; Alphaproteobacteria; Rhizonatoria
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WORMPEP; Y50E8A.16; CE24404.
InterPro; IPR003593; AAA, AIPase.
InterPro; IPR001140; ABC_TM_transpt.
InterPro; IPR003439; ABC_transporter.
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investigating biology.";
Science 282:2012-2018(1998).
TMTT.BRITY: BELONGS TO THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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SWART; SM00382; AAA; T.
PROSITE; PS00211; ABC TRANSPORTER; 1.
ATP-binding; Transport
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Pfam; PF00005; ABC_tran; 1.
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 SEQUENCE FROM N.A.

MEDLINE=21608550; PubMed=11743193;

Wood D.W., Setubal J.C., Kaul R., i

Okura V.K., Zhou Y., Chen L., Wood
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                        Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
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d G.E., Almeida N.F. J
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XA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
AA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
AA Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
AA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
AA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
AA Cielo C., Slater S.;
AC Cielo C., Slater S.;
Tenone sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
Science 294:2323-2328(2001).
Science 294:2323-2328(2001).
Science 294:2323-2328(2001).
Science 394:2323-2328(2001).
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EMBL; AUZ78573; CAC20926.1; -.
EMBL; AUZ78573; CAC20926.1; -.
HSSP; P18676; 1B4V.
InterPro; IPR000172; GMC oxred.
InterPro; IPR000311; Tat.
ITGREAMS; TIGR01409; TAT signal ser
ITGREAMS; PS00623; GMC OXRED 1; I
PROSITE; PS00623; GMC OXRED 1; I
PROSITE; PS00623; GMC OXRED 1; I
S49 AA; 59475 MW; 967
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Q9EW96;
Q9EW96;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINB=20547899; PubMed=11094342;

Aparicio J.F., Fouces R., Mendes M.V., Olivera N., Martir

Aparicio J.F., Fouces R., Mendes M.V., Olivera N., Martir

Aparicio J.F., Fouces R., Mendes M.V., Olivera N., Martir

Aparicio J.F., Fouces R., Mendes M.V., Olivera N., Martir

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Begins Involved in the biosynthesis of the 26-membered

genes is involved in the biosynthesis of the 26-membered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces natalensis.
Bacteria; Actinobacteridae; Actinomycetales;
Streptomycinaae; Streptomycetaceae; Streptomyces.
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Pred. No. 60;
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SPECIES-S.aureus (strain Mu50), and S.aureus (strain N315);

SPECIES-S.aureus (strain Mu50), and S.aureus (strain N315);

MEDLINE-21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi J.

Cui L., Oguchi A., Aoki K.-I., Nagqai Y., Lian J.-Q., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutanii-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Sh:

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus

aureus.";

aureus.";
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Q92214;
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SPECIES=S.aureus; STRAIN=SA502A;
MEDLINE=97342847; PubMed=9197262;
Ji G., Beavis R., Novick R.P.;
"Bacterial interference caused by
Science 276:2027-2030(1997).
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AGRD OR SAV2037 OR SA1842.1
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EMBL; AF001702; AAB63265.1; -.

EMBL; AF003364; BABE56199 1; -.

EMBL; AF003135; BAB43124.1; -.
Lu B.C.;
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Eukaryota; Fungi; Basidiomycota; Hym
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                           Cooper D.N.W.,
Lu B.C.;
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NCBI_TaxID=5346;
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                                                                 Boulianne R.P.,
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                                                                 Charlton S., Farrell E.,
   specificity
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                                                                                                                                                                                                                                                            Hymenomycetes; Homobasidiomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
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Kaito C.,
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RESULT
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Best Local S
Matches 7
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Best Local (
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Submitted (JUL-1996) to the EMB;
EMBL; U64676; AABO6178.1; -.
InterPro; IPR001079; Galectin.
pfam; PF00337; Gal-bind_lectin;
SMART; SM00276; GLECT; 1.
                                                                                                                                                                                                                                                                                                                                                 Q9ZVU6;
Q9ZVU6;
01-MAY-1999
01-MAY-1999
01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-jingxil7, and cv. Japonica; TISSUE=Shoot;
Yu F., Zhang A., Zhang F., Chen S.;
Yu F., Zhang A., Zhang F., Chen S.;
"Rice probable tyrosine phosphatase.";
Submitted (NAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF272978, AAF811798.1; -.

EMBL; AF272978, AAF811798.1; -.

HSSP; Q12923; 3PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice)
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2002 (TrEMBLrel. 22, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative tyrosine phosphatase (Fragment).
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                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; edicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gramene; Q9LKK3; -
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   Federspiel N.A., I
Altafi H., Araujo
                                                                                                                                                                                                                                                                                               T5A14.12 protein.
T5A14.12.
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                                                                      SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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9 (TrEMBLrel. 10,
2 (TrEMBLrel. 20,
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          Palm C.J., (
o R., Huizar
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          Conway A.B.,
r L., Rowley
                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
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          D.
                Conn L., Hansen
D., Buehler E., 1
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eudicots; Rosio
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RESULT OF SERVICE SOLUTION OF SERVICE SOLUTION
RESULT 10
Q8L972
ID Q8L97
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Best Local S
Matches 6
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Best Local S
Matches 6
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P YAMAGA K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee J A Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee J A Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G., A Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P., A Southwick A., Davis R.W., Ecker J.R., Theologis A.;

T "Arabidopsis Open Reading Frame (ORF) Clones.";

L Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY039926; AAK64030.1; -.

R EMBL; AY079359; AAL85090.1; -.

R InterPro; IPR001470, TPR.

R InterPro; IPR001470, TPR.

R InterPro; IPR001470, TPR.

R InterPro; PS50106; PDZ; 1.
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SEQUENCE FROM N.A.

Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

Pale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M.,

Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P.,

Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,

Karlin Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,

Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,

Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,

Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,

"Full Length cDNA of gene TSA14.12 (GI:4204267).";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
17-01-DEC-2001 (TrEMBLrel. 23, Last annotation update)
17-01-DEC-2003 (TrEMBLrel. 13, Last annotation update)
17-01-DEC-2003 (TrEMBLrel. 19, Last sequence of the update)
17-01-DEC-2003 (TrEMBLrel. 19, Last sequence update)
17-01-DEC-2003 (TrEMBLrel. 19, Last
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Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia
Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005223; AAD10648.1; -.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001440; TPR.
PROSITE; PS50106; PDZ; 1.
        Q8L972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 335 AA; 37410
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Pred. No. 78;
1; Mismatches
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Pred. No. 74;
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        PRT;
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01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

ONET TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Full-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
EMBL; AV088606; AAM66135.1;
InterPro; IPR001478; PDZ.
InterPro; IPR001479; TPR.
PROSITE; PS50106; PDZ; 1.
Hypothetical protein.
Hypothetical protein.
SEQUENCE 335 AA; 37456 MW; 1695924929A8F1B;
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Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alex
Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve
annotation.";
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Arabidopsis thaliana (Mouse-ear
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Lin X., Kaul S., Town C.D., Utterback T.R., Barnstead
Bowman C.L., White O., Nierman W.C., Fraser C.M.,
"Arabidopsis thaliana chromosome III BAC F978 genomic sequen
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC009991; AAF01509.1;
                                                                                                                                                                                                                                                                         SEQUENCE
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7; Conserv
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                                                                                                                                                                                                                                                                            356 AA;
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Pred. No.
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RA Fartmann B., Valle G., Bloecker H., Perez Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Fuigdomenech P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottler P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottler P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Winchach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Wezzi A., Drangelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conzed A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Ronard A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA Ronard A., Houdie M., Berger-Llauro C., Purnelle B., Masuy D.,
Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Ronney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Ronayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Pai G., Militscher J., Salbers S.L., White O., Venter J.C.,
RA Rasmoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Nisyama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
Fhaliana M., Wasuda M., Yasuda M., Tabata S.,
Fraser C.M., Kaneko T., Nakawahima K., Kishida S.,
Fraser C.M., Kaneko T., Nakawahima K., Kishida S.,
Fhaliana M., Wasuda M., Yasuda M., Tabata S.,
Fraser C.M., Kaneko T., Salber S., Takeuchi C., Wada T.,
Fraser C.M., Kaneko T., Salber S., Takeuchi C., Wada T.,
Fraser C.M., Kaneko T., Salber S., Takeuchi C., Wada T.,
Fraser C.M., Kaneko T., Salber S., Takeuchi C., Wada T.,
Fraser C
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Best Loc
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                                                                          Q9AT39;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
SHOOT1 protein.
SHOOT1.
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01-JUN-2001
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core evenosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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Glycine max (Soybean).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                          Q9AT39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature
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AC073395; AAG50971.1;
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Seki M., Iida K., Satou M., Sakurai T., Akiyama Seki M., Iida K., Satou M., Sakurai T., Akiyama Nakajima M., Enju A., Kamiya A., Narusaka M., Ca Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ da EMBL, AKI18481, BAC43085.1;
Hypothetical protein.
SEQUENCE 371 AA; 41708 MW; EAE35CC1DEB6321B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Karakaya C.H., Knap H.;

Submitted (FEB-2001) to the E
EWBL; AF349572; AAX37555.1;

Interpro; IPR001440; TPR.

SEQUENCE 359 AA; 40243 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                            O17485;
O17485;
O1-JAN-1998
O1-JAN-1998
O1-MAR-2003
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01-MAR-2003
01-MAR-2003
01-MAR-2003
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AT3G11150/F11B9 109.
Arabidopsis thaTiana (Mouse-ear cress).
Arabidopsis thaTiana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                     Aminopeptidase.

Plodia interpunctella (Indianmeal moth).

Plodia interpunctella (Indianmeal moth).

Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Eukaryota, Endopterygota, Lepidoptera, Glossata, Ditrysia, Pyr Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Pyr Pyralidae, Phycitinae, Plodia.
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   STRAIN=HD198-R;

MEDLINE=20195127; PubMed=10732989;

Zhu Y.C., Kramer K.J., Oppert B., Dowdy A.K.;

"CNMAs of aminopeptidase-like protein genes from Plo
"CNMAs of aminopeptidase-like protein genes from Plo
strains with different susceptibilities to Bacillus
                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                    NCBI_TaxID=58824,
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A., Narusaka M., Carninci P.,
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RI Insect Biochem. Mol. Biol. 30:215-224(2000).

DR EMBL, AF034484; AAC36147.1; -.

DR MEROPS; MOl.013; -.

DR InterPro; IPR001930; Ala peptase.

DR InterPro; IPR006025; Zn_MTpeptdse.

DR PINTS; PF01433; Peptidase M1; 1.

DR PRINTS; PR00756; ALADIPTAGE.

DR PROSITE; PS00142; ZINC_PROTEASE; 1.

SQ DESCIPTION OF STANDIPTAGE.

DR PROSITE; PS00142; ZINC_PROTEASE; 1.

SQUENCE 1016 AA; 115070 MW; C8D82D1FC582B33A CRC64;

SQUENCE 1016 AA; 115070
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Sequence 436, App
Sequence 18282, A
Sequence 40, Appl
Sequence 41, Appl
Sequence 71, Appl
Sequence 7, Appli

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Title:
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Sequence:
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US-08-861-476C-3
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US-07-9339-511-5
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APPLICANT: Moi. 6337385ick, Richard P.
APPLICANT: Mo. 6337385ick, Richard P.
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
CURRENT FILLING LOTE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 9
TYPE: PRI
CORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
OCHER INFORMATION: Description of Artificial Sequence: Synthetic
NAME/KEY: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position.
US-09-339-511-4
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US-09-339-511-1
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US-09-339-511-4
                                                                                                                                               Sequence 1, Application Patent No. 6337385 GENERAL INFORMATION:
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      Muir, Tom
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No. 6337385ick, Ricl
Beavis, Ronald
Ji, Guangyong
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US-09-240-274-42
US-09-252-991A-18282
US-08-118-270-40
PCT-US93-08528-40
US-09-116-872A-17
US-09-115-418-5
US-09-115-418-5
US-09-171-035-116
US-08-484-575A-7
US-08-484-575A-7
US-08-484-575A-7
US-08-484-575A-7
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US-08-484-575A-7
US-08-484-575A-7
US-08-485-414-7
PCT-US94-01826A-7
PCT-US94-01826A-7
PCT-US94-01835-114
US-07-955-905A-26
                                                                       Richard
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Result No.

Minimum Maximum

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OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide; NAME/KEY: VARIANT; LOCATION: (5)
COTHER INFORMATION: Xaa represents any amino acid at this position US-09-339-511-1
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Best Local Similarity
Thes 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT ; ORGANISM: Staphylococcus aureus US-08-861-476C-3
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                                            CURRENT APPLICATION NUMBER: US/08/861,476C
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.0 SEQ ID NO 3 LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE: 63753/7
CURRENT APPLICATION NUMBER: US/08/861,476C
CURRENT FILING DATE: 1997-05-22
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Best Local
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                                                                                                                                                                                           Sequence 6, Application US/08861476C
Patent No. 6447786
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Patent No. 6447786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 8
                                                                                                                                             APPLICANT: New York University Medical Center TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
ORGANISM: Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
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                                                                                                                                 REFERENCE: 63753/7
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milarity 100.0%;
Conservative
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Pred. No. 2.5e
0; Mismatches
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Pred. No.
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LENGTH: 426
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Best Local :
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; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/198,452A CURRENT FILING DATE: 1998-11-24
TELEFAX: 312 616-5460
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Chlamydia pneumoniae genomic TITLE OF INVENTION: thereof and uses thereof, in TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 616-5400
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            CITY: Chicago
                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                      PPLICATION NUMBER: US
ILING DATE: 19901012
LASSIFICATION: 800
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                                                          Gamson, Edward P
                                                                                                                                                                                                                                                                                                                                                 INVENTION: Method and INVENTION: Sterol Accu
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                                                                                                                                                                                                                                                          Illinois
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Accumulation in
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Pred. No. 1
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6.3;
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Higher Plants
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US-07-934-374-4
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                                                                       US-07-783-861C-2
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             Sequence 2, Application US/07783861C Patent No. 5460949
GENERAL INFORMATION:
                                                                                                                                                                                                                  Matches
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APPLICANT: Chappe
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1054 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC compatible
COMPUTER: PC compatible
COMPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,374
FILING DATE: 1920814
CLASSIFICATION: 800
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LENGTH: 1054 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 616-5400
TELEPAX: 312 616-5460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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APPLICANT: Wolf, Fred R.
TITLE OF INVENTION: Process and Composition for Increasing
TITLE OF INVENTION: Sterol Accumulation in Higher Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chappell, J.
APPLICANT: Saunders, Cou
APPLICANT: Cuellar, R.
APPLICANT: Wolf, Fred R.
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                      LENGTH: 1054 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                Local Similarity
les 6; Conserv
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                                                                                                                                            226 VNSASSLF 233
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180 N. Stetson St.
Saunders,
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75.0%;
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75.0%;
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Pred. No. 3
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Pred. No. 3
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3.2e+02;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,380
PILING DATE: 15-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: GALLOWAY, NO. 5460949Vall B.
TELECOMMUNICATION INFORMATION:
TELEPAX: 312 856-7180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-339-511-5
                                                                                                              SOFTWARE:
SEQ ID NO 5
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                             APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILLING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR SIEQ ID NOS: 8
NUMBER OF SIEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: No. 6337385ick, Richard P.
                                             TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60680-0703

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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LENGTH: 1054 amino aci
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Local Similarity 75.0%;
les 6; Conservative
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STATE: Illinois
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FILING DATE: 19911028
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5. 6337385
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                                                                                                                                                                                                                                                                                                                                                                                                 Beavis, Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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200 East Randolph St.
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Pred. No.
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US-09-339-511-6
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TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PI
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEO ID NOS: 8
NUMBER OF SEO ID NOS: 8
                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Richard
APPLICANT: No. 6337385ick, Richard
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
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                                                                                                                                                                                                                                                               Sequence 2, Application US/09339511 Patent No. 6337385
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APPLICANT: Mayville, Patricia
APPLICANT: No. 633738510k, Richard P.
            CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
                                                                                          APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRGANISM: Artificial Sequence
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PatentIn Ver. 2.0
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Q ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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87.5%;
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87.5%;
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Pred. No.
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Pred. No. 2.5e+05;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 518
; TYPE: PRT
; ORGANISM: SIV - viral
US-09-625-972-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5) OTHER INFORMATION: Xaa represents any amino US-09-339-511-2
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Best Local Similarity bo...
6; Conservative
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                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23, Appl:
Patent No. 656651
SEQ ID NO 27566
LENGTH: 762
                                                                                                                                                                                                                                                              Sequence 27566, Application US/09252991A Patent No. 6551795
                              APPLICANT: MARC J. Rubenfield et al.

APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING PILLS OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION STEEL 1998-07-77

NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2000-07-29
PRIOR APPLICATION NUMBER: DE 199 36 003.0
PRIOR FILING DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GUERTLER, Lutz Gerhard
APPLICANT: HAUSER, Hans Peter
APPLICANT: DONGMO DELOXO, Yvette Beatrice
APPLICANT: ZEKENG, Leopold
APPLICANT: XAPFUE, Lazare
TITLE OF INVENTION: LENTIVIRUS FROM THE GROUP
TITLE OF INVENTION: (MANDRILLUS LEUCOPHAEUS)
FILE REFERENCE: 067559/0106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/625,972 CURRENT FILING DATE: 2000-07-29
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Pred. No. 3.9e
1; Mismatches
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Pred. No.
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Query Match
Best Local Similarity
"^+^hes 6; Conserva
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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US-09-339-511-7
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                                                                                                                                                                                                                                                                                                                                               ; TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-451-12
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US-08-477-451-12
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                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches ·5
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SEQUENCE CHARACTERISTICS:
LENGTH: 1720 aming
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                                                                                                                    Sequence 7, Application US/09339511
Patent No. 6337385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Covacci, Antonello
TITLE OF INVENTION: Helicobacter Pylori Cagi Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 033
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/477,451 FILING DATE: 07-UN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94608-2916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 4560 Horton Street CITY: Emeryville
                                                                                                                                                                                                                    1664 INATOSLF 1671
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                                                                                                      INFORMATION:
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Similarity 62.5%;
5; Conservative
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                                          Mayville, Patricia
No. 6337385ick, Richard P.
Beavis, Ronald
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Guangyong
ION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
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Pred. No. 6e+0
0; Mismatches
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Pred. No. 1.5e+03;
1; Mismatches 2;
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6e+02;
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                                                                                                                          , OTHER INFORMATION: Xaa represents any amino acid at this position. US-09-339-511-7
                                                                                                                                                                                                                                                                   SOFTWARE:
SEQ ID NO 7
LENGTH: 9
                                                             Matches
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                 PILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                      OTHER INFORMATION:
OTHER INFORMATION:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                     FEATURE:
                                                  Local Similarity 87.5%; hes 7; Conservative
2 VNAXSSAF 9
                            2 VNAXSSLF 9
                                                                                                                                                                                                                                                                                                  PatentIn Ver. 2.0
                                                                                                                                                                                     Description peptide
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                                                           Score 26; DB 4; Pred: No. 2.5e+05; 0; Mismatches 1
                                                                                                                                                                                                        of Artificial Sequence: Synthetic
                                                                                           Length 9;
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Search completed: January 29, 2004, 15:03:21 Job time: 11.1176 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                  Score
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seq length:
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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37
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[2] (Ggn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: (Ggn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: (Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: (Ggn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
5: (Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
6: (Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
6: (Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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 AVNAXSSLF 9
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Copyright (c) 1993 - 2004 Compugen Ltd
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/ Cgn12_6/ptodata/1/pubpaa/US08A_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
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US-10-369-493-6225
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US-10-201-444-6
US-09-919-781-2
US-10-289-762-760
US-10-289-762-760
US-10-369-493-1849
US-10-369-493-1849
US-10-369-493-1860
US-10-369-493-14564
US-10-369-493-14564
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Sequence 1,2
Sequence 3,
Sequence 6,
Sequence 1,3
Sequence 13,
Sequence 1760
Sequence 1184
Sequence 1,8
Sequence 1,8
Sequence 1,8
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Sequence
                                                   2, Appli
13, Appl
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6225, Ap
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US-10-032-950-4

Sequence 4, Application US/10032950 Publication No. US20020077453A1

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equence 2024, A	ce 436	equence 436, Ap	equence 877, Ap	equence 22496	equence 21095	equence 255,	equence 10, F	equence 218,	equence 733,	equence 6990,	equence 9876,	equence 4143,	equence 7, Ap	equence 11, 1	equence 11, A	equence 2, Ar	equence 1, Ap	equence 6788,	equence 23,	equence 31, A	equence 12, A	equence 37, A	equence 14, A	equence 27613	equence 2, Ap	equence 138,	equence 3924,	equence 2265,	equence 114

ALIGNMENTS

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Best Local S
Matches
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TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: No. U820020077453Alick, Richard
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
                                                                                                                                                            OTHER INFORMATION: Description of Artificial SequOTHER INFORMATION: peptide
NAME/KEY: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid
                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                      Similarity 100 9; Conservative
                         AVNAXSSLF 9
 AVNAXSSLF
                                                                                         94.6%;
100.0%;
                                                                      0;
                                                                                         Score 35; pred. No.
                                                                                                                                                                                                                                        of Artificial Sequence: Synthetic
                                                                          Mismatches
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7e+05;
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; OTHER INFORMATION: Xaa represents any amino acid at this position US-10-032-950-1
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APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: FLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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US-10-369-493-6225
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SEQ ID NO 6225
LENGTH: 633
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SEQ ID NO 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL TITLE OF INVENTION: INTERFERENCE FILE REPERENCE: 600-1-231N CURRENT APPLICATION NUMBER: US/10/032,950 CURRENT FILING DATE: 2001-12-27 CURRENT FILING DATE: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
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APPLICANT: No. US20020077453Alick, Richard
APPLICANT: Beavis, Ronald
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7; Conserve
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77.8%;
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k; Pred. No. 7e+
0; Mismatches
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Pred. No. 21;
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7e+05;
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TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201444-3
                                                                                                                                                                                                                   US-09-919-781-2
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Staphylococcus aureus US-10-201-444-6
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Sequence 2, Application US/09919781
PATENT NO. US20020123094A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: 57250, A NOVEL HUMAN SUGAR TRANSPORTER
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: MNI-181
CURRENT APPLICATION NUMBER: US/09/919,781
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US/09/919,769
PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10201444

Publication No. US20030078378A1

GENERAL INFORMATION:
APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE: 63753/7
CURRENT APPLICATION NUMBER: US/10/201,444

CURRENT FILING DATE: 2002-07-23

CURRENT FILING DATE: 2002-07-23
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Publication No. US20030078378A1
GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN:
FILE REFERENCE: 63753/7
CURRENT APPLICATION NUMBER: US/10/201,444
CURRENT FILING DATE: 2002-07-23
FRIOR APPLICATION NUMBER: US/08/861,476
PRIOR PRIOR DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
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PRIOR APPLICATION NUMBER: US/08/861,476
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
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TYPE: PRT
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nes 7; Conservative
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0; Mismatches
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Pred. No.
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US-10-289-762-760
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                                                                          ; TYPE: PRT ; ORGANISM: Chlamydia US-10-289-762-760
                                                                                                                          Sequence 760, Application US/10289762
Publication No. US20040006218A1
GENERAL INFORMATION:
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REPERENCE: 9710-003-99
FULE REPERENCE: 9710-003-99
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATS: 2003-03-27
NUMBER OF SEQ ID NO5: 6849
SEQ ID NO 760
LERGTH: 426
TYDE: DET
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 572
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Curtis, Rory A.J.
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Meyers, Rachel E.
APPLICANT: Meyers, Rachel E.
APPLICANT: Meyers, Rachel E.
APPLICANT: Meyers, Rachel E.
TITLE OF INVENTION: 57259, 671118, 67067, 62092, 8099, 46455, 54414, 53763,
TITLE OF INVENTION: 67076, 67102, 44181, 67084FL, 67084ALT, FBH58295FL, 57255,
TITLE OF INVENTION: AND 57255alt MOLECULES AND USES THEREFOR
FILE REFERENCE: MMI-249
CURRENT APPLICATION NUMBER: US/10/154,419
CURRENT APPLICATION DATE: 2002-05-22
CURRENT FILING DATE: 2002-05-22
CURRENT FILING DATE: 2002-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 572
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lication No.
Local Similarity 66.
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                                                                                             pneumoniae
                  78.4%;
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77.8%;
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Pred. No. 1.5e+02;
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Pred. No. 1.5e+02;
1; Mismatches
                  Score 29; DB 12;
Pred. No. 1.9e+02;
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                                     Length 426;
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Sequence 5, Application US/10032950
publication No. US20020077453A1
GENERAL INFORMATION:
APPLICANT: Mur. Tom
APPLICANT: Mayville, Patricia
                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Saccharomyces cerevisiae US-10-369-493-1849
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US-10-369-493-1849
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US-10-100-303A-110
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US-10-100-303A-110
                                                                                                    RESULT 11
US-10-032-950-5
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CURRENT APPLICATION NUMBER: US/10/100,303A
CURRENT FILING DATE: 2002-03-18
NUMBER OF SEQ ID NOS: 138
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Publication No. US20030202980A1
GENERAL INFORMATION:
APPLICANT: Caplan, et al.
TITLE OF INVENTION: Methods and Reagents for Decreasing
TITLE OF INVENTION: to Allergy
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US(10/369,493
CURRENT APPLICATION NUMBER: US(10/369,493
CURRENT APPLICATION NUMBER: US(10/369,493
CURRENT APPLICATION NUMBER: US(10/369,493
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US(10/360,039)
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1849, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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Best Local
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Local Similarity 75.0%;
hes 6; Conservation
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                                                                                                                                                                                                                                                                                         78.4%;
75.0%;
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Pred. No. 2
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Query Match
Best Local Similarity
Watches 7; Conserve
                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide; NAME/KY: VARIANT; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position US-10-032-950-6
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FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.0
                                                                                        Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453A1ick, Richard
APPLICANT: Beavis, Ronald
APPLICANT: Francong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
                                                                                                                                                                                                                                                            LENGTH: 9
TYPE: PRT
CORGANISM: Artificial Sequence
FEATURE:
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                                                                        . Similarity 7; Conserv
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                                    VNAXSSLF 9
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Beavis, Ronald
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87.5%;
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Pred. No.
                                                                                          Score 28; DB 13; Pred. No. 7e+05;
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7e+05;
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US-10-078-929-136
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SEQ ID NO 136
LENGTH: 78
                                                                                                                                                                                                                                                                                  Sequence 14264, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved TITLE OF INVENTION: Stress Response FILE REFERENCE: BB1357 US NA CURRENT APPLICATION NUMBER: US/10/078,929 CURRENT FILING DATE: 2002-02-19
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILLE OF INVENTION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/60,039
PRIOR APPLICATION NUMBER: US/60/360,039
PRIOR APPLICATION DATE: 2003-02-21
PRIOR PRIOR DATE: 2003-02-31
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                    -10-369-493-14264
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PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 208
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PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION UNMBER: 60/133436
PRIOR FILING DATE: 1999-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
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FILING DATE: 1999-05-11
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FILING DATE: 1999-05-11
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Thorpe, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Famodu, Omos
Odell, Joan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Falco, Saveri
Sakai, Hajime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NG DATE: 2002-02-19
ATION NUMBER: 09/566,394
DATE: 2000-05-05
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b. US20020152497A1
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75.0%;
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Pred. No. 50;
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RESULT 15
US-10-369-493-14770
(Sequence 14770, Application US/10369493)

Publication No. US20030233675A1

GENERAL IMFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Glater, Steven C.
APPLICANT: Glater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52052) B
CURRENT ELIUNG DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US/10/369,493

CURRENT ELIUNG DATE: 2002-02-21
NUMBER OF SEQ ID NO 14770
LENGTH: 248
TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14770
Search completed: January 29, 2004, 15:01:45 Job time: 25.5441 secs
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; TYPE: PRT
; ORGANIAM: Agrobacterium tumefaciens
US-10-369-493-14264
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Post-processing: Minimum Match 0%
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ABP53544
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ALIGNMENTS

Staphylococcus aureus infection; cyclic peptide; AgrD; agr response; virulence factor; treatment. Staphylococcus aureus S. aureus peptide #5 used for bacterial interference. AAY67855 standard; peptide; 9 AA (first entry) ROCKEFELLER. NEW YORK STATE 98US-0103438 99WO-US14562 5 /label= Unknown /note= Location/Qualifiers "N-terminal residue forms residue to form a cyclic bond with C-terminal peptide"

Result

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RESULT 2
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The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is a secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. Preferred peptides may have the sequence NH2-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z residue and COOH other than a thioester
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                    This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
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Pred. No. 9.3e+05;
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The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AAM50899-906). The peptide corresponds to the Staphylococcus aureus AgrOII sequence with a Cys5 to Ser mutation (lactone). It was synthesised on a Wang-resin using an Fmoc N-alpha protection stratesy. Following chain assembly, the peptide was cleaved from the support and the Ser-5 residue deprotected by treatment with a trifluoroacetic acid smisole:water mixture (90:5:5) for 4 hr. The partially protected peptide-alpha (90:5:5) for a trifluoroacetic acid smisole:water mixture carboxylates were then dissolved in DMF and treated with PyBOP and a catalytic amount of dimethylaminopyridine. Cyclization was complete after 2 hr. The remaining protecting groups were then removed by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the agr response of Staphylococcus aureus. The thiololactone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure with a lactone (as in the present case) or a lactam can component of the cyclic ring structure with a lactone (as in the present case) or a lactam can component of the cyclic ring and component of the cyclic ring and component of the cyclic ring and component of the cyclic and can component of the cyclic activation activity while preserving and component of the cyclic activation of this cyclic sectul for infection.
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infection; therapy; cyclic.
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Query Match Best Local Similarity

89.7%; 77.8%;

Score 35; Pred. No.

DB 23; 9.3e+05;

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1 GVNAXASLF Similarity 7; Conserv

Matches Query Match

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                                                                             The present sequence is that of a novel synthetic AgrD2 linear thioster peptide. The peptide is derived from the cyclic AgrD2 agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrP3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone cyclic peptide (see AAMS1001), the present peptide was unable to either activate or inhibit the agr response to be dither activate or inhibit the agr response to be dither activate or inhibit the agr response to be dither activate or inhibit the agr response, even when added to cultured cells at uM concentrations. The invention when added to cultured cells at uM concentrations. The invention and methods for preparing them. The cyclic peptides are useful for infection interference, especially for the treatment of S. aureus
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                                                                                                                                          Query Match
Best Local
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                                                                                                                                                                                                                              Sequence
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AIND
                                                                                                               Similarity 7; Conser
                                                       GVNAXASLF 9
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                                                                                                                  Conservative
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NEW YORK STATE
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                                                                                                                                          89.7%;
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                                                                                                               Score 35; DB
Pred. No. 9.3e
1; Mismatches
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                                                                                                                                       DB 23;
9.3e+05;
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                                                                                                                   The present sequence is that of a novel synthetic AgrD2 lactone cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactone bond. The peptide is derived from an AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrD2 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. The lactone AgrD2 peptide inhibited the agr response in group I. I or III strains without activating the agr response in group I. II or III captains. The invention provides claimed cyclic peptides (see AMS0899-906 and AAMS0999) and methods for preparing them, especially peptides where the cyclic bond is a lactam or lactone bond. The cyclic peptides are useful for bacterial interference,
                                                 Matches
                                                           Query Match
Best Local
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                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                               Example 1; Column 9; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        subject
                                                                                                                                                                                                                                                                                                                                                                                                   Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-170774/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muir TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUN-1998;
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UNIV NEW YORK STATE.
                                               Similarity 7; Conserv
                         GVNAXASLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   response; inhibitor; antibiotic; antibacterial; therapy; lactone; cyclic.
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                                                 Conservative
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                                                           89.7%;
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                                               Score 35; DB;
Pred. No. 9.3e-
1; Mismatches
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                                                                          DB 23;
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RESULT 9
AAM51004
ID AAM5

AAM51004 standard; Peptide; 9

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RESULT 11
AAY67851
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of autoinducer-2 agonists or antagonists autoinducer-2 receptor, regulating bacterial also antibiotic compositions
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Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;
                          S. aureus peptide #1 used for bacterial interference.
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 33; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bassler BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYPR-)
(QUOR-)
(UYTE-)
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07-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vulnerary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB07160 standard; peptide;
                                                      25-APR-2000
                                                                                  AAY67851;
                                                                                                         AAY67851 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                  quorum sensing.
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QUOREX PHARM INC
UNIV TECHNOLOGIE
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                                                                                                                                                                                                        GVNAXASLF
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2000US-254398P
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                                                      (first entry)
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                                                                                                                                                                                                                                               89.7%;
77.8%;
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                                                                                                                                                                                                                                 Score 35; DB 23;
Pred. No. 9.3e+05;
1; Mismatches 1
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                                                                                                                                                                                                                                                          Length 9;
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RESULT 12
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XX Staph
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XX Staph
XX Wirul
XX Wisc-
FT Misc-
FT Misc-
FT W0996
XX W0996
XX 29-DE
XX 24-Jt
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a cyclic peptide derived from the Staphylococcus aureus AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virulence factor; treatment
                                                                                                                                                   Staphylococcus aureus infection; AgrD; agr response; treatment; virulence factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 26; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cyclic peptides for treating infections with Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muir TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-1999;
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                                                                                                                           Staphylococcus
                                                                                                                                                                                      Staphylococcus
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                                                                                                                                                                                                                                                                AAY67861 standard; peptide;
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                         29-DEC-1999.
                                                   WO9967286-A2
                                                                                        Misc-difference
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8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA;
                                                                                                                                                                                                                (first entry)
                                                                                                                           aureus
                                                                                                                                                                                         aureus
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                                                                           Location/Qualifiers
5
/label= Unknown
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                                                                                                                                                                                        AgrDII derived peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novick RP,
                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 21;
Pred. No. 9.3e+05;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ji G,
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 9
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24-JUN-1999;

99WO-US14562

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RESULT 13
ABP53540
ID ABP53540
ID ABP53
XX ABP53
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Best Local S
Matches 8
                                                                                      (MUIR/) MUIR T W.
(MAYV/) MAYVILLE F
(NOVI/) NOVICK R F
(BEAV/) BEAVIS R.
(JIGG/) JI G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP53540;
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    WPI; 2002-681366/73
                                                                                                                                                                                                                          24-JUN-1998;
24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyclic
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                                               Muir TW,
                                                                                                                                                                                                                                                                                          27-DEC-2001; 2001US-0032950
                                                                                                                                                                                                                                                                                                                                                                              US2002077453-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agr response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
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8; Conserv
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                                               Mayville P,
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NEW YORK STATE.
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99US-0339511
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus; infection; antibacterial;
                                                                                                                                   ש. ה.
                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "any amino acid"
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88
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                                                 Novick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB:
Pred. No. 9.3e.
1; Mismatches
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9.3e+05;
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Best Local S
Matches
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                                                  Novel synthetic, interference and subject -
                                                                                                     Muir
                                                                                                                    (UYRQ )
                                                                                                                                                                              08-JAN-2002.
                                                                                                                                                                                                US6337385-B1
                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                    antibacterial;
                                                                                                                                                                                                                                                                                                                           Staphylococcus
                                                                                                                                                                                                                                                                                                                                           AgrD-autoinducing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 10; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New cyclic peptides, useful infections -
                                 Claim 7;
                                                                                                                                              24-JUN-1998;
                                                                                                                                                             24-JUN-1999;
                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as an agr gene response inhibitor. The peptides are ting S. aureus infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                  Column 19;
                                                                                                    Mayville P,
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                                                                                                                     ROCKEFELLER.
NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                  aureus; AgrD; agr response; inhibitor; antibiotic;
infection; therapy; cyclic.
                                                                                                                                              98US-090402P
                                                                                                                                                              9908-0339511
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                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                         cyclic AgrD-autoinducing peptide for bacterial for treating Staphylococcus aureus infection i
                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                           cyclic peptide,
                                                                                                                                                                                                                                                                                                                                                                                              Peptide;
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                                 18pp; English.
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                                                                                                     Novick RP,
                                                                                                                                                                                                             "note linked to residue peptide"
                                                                                                                                                                                                                                       "note linked to peptide"
                                                                                                                                                                                                                                                                "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                               ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for treating Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 23;
Pred. No. 9.3e+05;
1; Mismatches 0;
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The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response staphylococcus aureus. It is an AgrD-autoinducing peptide, when

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RESULT 15
AAM/50908
ID AAM/50908
AC AAM/50
AC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protected peptide used in cyclic peptide production.
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                                                                24-JUN-1998;
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         (UYRQ ) UNIV ROCKEFELLER
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infection; therapy; cyclic.
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                                                                98US-090402P
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Ser(Bzl)"
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                                                                                                                                                                                                                                                                                                                                                                                        note linked peptide"
                                                                                                                                                                                                                                                                                                    "note linked to peptide"
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Pred. No.
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9.3e+05;
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Search completed: January 29, Job time: 35.0735 secs

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The present sequence is that of a protected peptide used in an acceptance of the preparation of novel synthetic cyclic peptides of the invention (see AAM50899-906). The peptide corresponds to the Staphylococcus aureus AgrDII sequence with a Cys5 to diaminopropionic carid (Dpr) mutation (lactam). It was synthesised on a Wang-resin cusing an Fmoc N-alpha protection strategy. Following chain assembly, the peptide was cleaved from the support and the Dpr-5 residue deprotected by treatment with a trifluoroacetic acidianisole:water carboxylates were then dissolved in DMF and treated with PyBOP. Cyclization was complete after 2 hr. The remaining protecting groups cover removed by treatment with HF and the peptide purified by HBLC. CR The cyclic peptide is capable of inhibiting the agr response of Staphylococcus aureus. The thiolactone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring cstructure with a lactam (as in the present case) or a lactone can can destructure with a lactam (as in the present case) or a lactone can confidency activity. The cyclic peptides are useful for charterial interference, especially for the treatment of S. aureus
Query Match
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Matches 8
                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection i
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Pred. No. 9.3e+05;
1; Mismatches 0;
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Listing first 45 summaries
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3: pir3:*
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39
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Gapop 10.0 , Gapext 0.5
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AC2563
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C89995
A28067
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B43715	A44942	D69805	E83194	AD1518	AD1159	D83354	T40120	T45786	T41065	G89189	H71562	T33320	EPFF	A53572	D97308
protein M homolog	fructose-bisphosph	iron(III) dicitrat	polyamine transpor	flagellar biosynth	Ď,	hypothetical prote	C2H2 type zinc fin	receptor-protein k	RNA binding protei	protein Y32F6A.3 [probable flageliar	hypothetical prote	zip protein precur	prostaglandin E2 r	probable membrane

ALIGNMENTS

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	RESOLUTE A RECOLUTE A RESOLUTE A
	C:Species: Bacillus subtilis (
	C:Accession: C69812
	R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
	A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
	A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henant, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
	Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
nce to have a	v. M.; Ogawa. K.; Ogiwara. A.; Oudeqa. B.; Park. S.H.; Parro, V.; Pohl, T.M.; Portete
ilt being printed,	Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
ibution.	A; Authors: Schleich, S.; Schroeter, R.; Scollone, F.; Sekiguchi, J.; Sekowska, A.; Se
	akeudni, m.; idmakoshi, k.; idmaka, i.; idiperid, f.; idgudni, k.; vaca, K.; voshida T.; Winters, P.; Winat, A.; Yamanoto, H.; Yamanoto, K.; Yashida, K.; Voshida
	A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
Description	A;Itte: The Complete genome sequence of the Stam Postative Macrestam Entitled Succession A;Reference number: A69580; MUID:98044033; PMID:9384377
	A;Accession: C69812
AGTD DIGITOME ABC ER	A; Molecule troe: DNA A: Molecule troe: DNA
lysosomal membrane	A; Residues: 1-333 <kun></kun>
P2B/LAMP-1 precurs	A;Cross-references: GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12580.1; PID:g26330
120K lysosomal mem	A:Experimental source: Strain 168
iron(III) dicitrat	C;Genetios: A;Genetios:
hypothetical prote	C;Superfamily: ferrichrome ABC transporter
farric exochalin "	94.9%;
transposase all700	
transposase all730	vative (
transposase all/11	Qy 1 GVMAXASLF 9
transposase all710	Db 99 GVNAGASIF 107
cytochrome-c oxida	
hymothetical prote	RESITT 2
probable glutamine	C89995
probable glutamine	AgrD protein [imported] - Staphylococcus aureus (strain N315)
transposase alr732	C/Species: Staphylococcus aureus G-hare- 10-may-2001 #semishore ravision 10-may-2001 #text change 22-Oct-2001
transposase all726	C;Accession: C89995
urease (EC 3.5.1.5	R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
iron (TTT) dicitra	ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, K.; Katuo, C.; Serimitu, K. C.; Shiba, T.; Hattori, M.; Oqasawara, N.; Hayashi, H.; Hizamatsu, K.
multidrug resistan	Lancet 357, 1225-1240, 2001
hypothetical prote	A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

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A;Reference number: A89758; MUID:21311952; PMID:
A;Accession: C89995
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-47 <KUR>
A;Cross-references: GB:BA000018; PID:g13701831;
A;Experimental source: strain N315
C;Genetics:
A;Gene: agrD
RESULT
A30200
                                                                                                                                                                                                                                                                                                           C;Accession: A60534
R;Heffernan, M.; Yousefi, S.; Dennis, J.W.
Cancer Res. 49, 6077-6084, 1989
A;Title: Molecular characterization of P2B/LAMP-1, a major protein target of a metastas:
A;Reference number: A60534; MUID:90002989; PMID:2676155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Chen, J.W.; Cha, Y.; Yuksel, K.U.; Gracy, R.W.; August, J.T.
J. Biol. Chem. 263, 8754-8758, 1988
A;Title: Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycoprote A;Reference number: A28067; MUID:88243732; PMID:3379044
A;Accession: A28067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-382 <CHE>
A;Cross-references: GB:J03881; NID:g198706; PIDN:AAA39411.1; PID:g293692
A;Cross-references: GB:J03881; NID:g198706; PIDN:AAA39411.1; PID:g293692
A;Note: the authors translated the codon ATT for residue 1 as Leu and CCG for residue 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lysosomal membrane glycoprotein LAMP-1 - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change C;Accession: A28067
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A; Residues: 1-405 < HEF >
C; Superfamily: lysosome
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Best Local
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|Species: Mus musculus (house mouse)
|Jate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 03-May-1996
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77.8%;
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Pred. No. 0.61
1; Mismatches
                                                                                                                                                 2; Mismatches
                                                                                                                                                                  Score 32;
Pred. No.
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A;Reference number: S74322; MUID:97061201; PM
A;Accession: S74439
A;Status: nucleic acid sequence not shown; tr
A;Molecule type: DNA
A;Residues: 1-349 < KANN>
A;Cross-references: EMBL:D90899; GB:AB001339;
A;Note: the nucleotide sequence was submitted
C;Genetics:
A;Gene: fecD
C;Superfamily: vitamin B12 transport protein
C;Keywords: iron transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iron(III) dicitrate transport system permease protein fecD - Synechocystis sp. (strai N;Alternate names: protein slr1317 C;Species: Synechocystis sp. 125-Apr-197 #text_change 20-Jun-2000 G;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000 C;Accession: S74439 C;Accession: S74439 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res 3, 109-136, 1996 Sp. 109-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X14765; NID:g56577; PIDN:CAA32873.1; A;Note: part of this sequence, including the amino end of the C;Superfamily: lysosome-associated membrane protein
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N;Alternate names: sialoglycoprotein
C;Species: Rattus norvegicus (Norvein
C;Date: 18-Oct-1989 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
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A;Note: the authors translated the codon GGG for residue 15
R;Hhmeno, M; Noguchi, Y.; Sasaki, H.; Tanaka, Y.; Furuno, F
FEBS Lett. 244, 351-356, 1989
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A;Residues: 22-407 <HIM>
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A; Residues: 1-407 < HOW>
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: Derived protein sequence, oligosaccharides, and membrane insertion of
113
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GVNAGASL
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87.5%;
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Pred. No.
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transposase alr8502 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120delta C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AC263
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Riference number: AB1807; MUID:21595285; PMID:11759840
A;Ricsession: AC263
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 173, 5771-5777, 1991
A;Title: Characterization of insertion sequence IS892 and related elements from the cyan
A;Reference number: A38116; MUID:91358369; PMID:1653218
A;Accession: B38116
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A;Experimental source: PCC 7120
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A,Molecule type: DNA
A,Residues: 1-188 <CAI>
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C;Date: 24-Jul-1992
C;Accession: B38116
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A;Reference number: Z19903
A;Accession: T24523
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A;Molecule type: DNA
A;Residues: 1-188 <KUR>
A;Cross-references: GB:AP003604; PIDN:BAB77421.1; PID:g17134865; GSPDB:GN00183
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C;Species: Anabaena sp.
C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 24-Nov-1999
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A;Map position: 4
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A;Experimental source: clone T05E11
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Best Local S
Matches 6
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Best Local S
Matches 7
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Pred. No.
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C;Accession: AD2478

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigunakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AD2478
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A;Gene: alr8502
                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-247 <KUR>
A;Cross-references: GB:HA000020; PIDN:BAB78088.1; PID:g17135542; GSPDB:GN00180
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                             transposase all7004 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alp
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
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A;Molecule type: DNA
A;Residues: 1-234 <FIS>
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Mol. Microbiol. 14, 557-569, 1994
A;Title: Identification of genes involved in the sequestration
A;Reference number: S60885; MUID:95191405; PMID:7885234
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C;Date: 27-Apr-1996 #sequence_revision
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C;Superfamily: Anabaena
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                                                                                                                                      C; Superfamily: Anabaena insertion sequence IS892 hypothetical protein
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R;Fiss, E.H.; Yu, S
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                                                                                                     Length 247;
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M.; Tabata
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transposase all7375 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120all C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AG2524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An. A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2491
C;Accession: A02524
C;Accession: A02524
R;Kaneko, T;, Nakamura, Y.; Wolk, C.P.; Kuritz, T.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transposase all7111 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha C;Species: Nostoc sp. PCC 7120 
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 
C;Accession: AC2491
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An. A;Reference number: AB1807; MUID:21595285; FMID:11759840
A;Accession: AF2515
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A,Molecule type: DNA
A,Residues: 1-247 <KUR>
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A;Experimental source: strain PCC 7120
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NA Res. 8, 205-213, 2001
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;Genome: plasmid
;Superfamily: Anabaena insertion sequence IS892 hypothetical protein
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;Superfamily: Anabaena insertion
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Best Local :
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Pred. No. 19;
2; Mismatches
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Pred. No. 19;
2; Mismatches
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    ; Sasamoto,
M.; Yamada,
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    S.; Watanabe, A.; Iriguch, M.; Yasuda, M.; Tabata,
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, M.; Yasuda, M.; Tabata, i
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Search completed: January 29, Job time: 11.1176 secs

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A;Status: PIL-1...A;Status: PILAAA;Molecule type: DNAA;Mesidues: 1-247 <KUR>A;Residues: 1-247 <KUR>A;Cross-references: GB:BA000020; PIDN:BAB78189.1;
                                                                                                                                                                                                                                                                                                                                                                                      transposase all7105 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. Strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AII490
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irig. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabat; DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21593285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:BA000020; IA;Experimental source: strain PCC C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-247 <KUR>
                                                                                                                                                                     A;Gene: all7105
A;Genome: plasmid
C;Superfamily: Anabaena insertion sequence IS892 hypothetical protein
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2524
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Best Local
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66.7%;
    72
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C 7120
                                                                                                          Score 30; DB 2; 
Pred. No. 19;
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Pred. No.
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Maximum Match 100%
Listing first 45 summaries
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DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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39
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    SwissProt_41:*
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    DB
                   ALF PLAFA
MX STRY

SELA HELPY

SELA HELPY

REM9-HUMAN
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SC24_YEAST

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P35408 homo sapien
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P42218 escherichia
O42218 homo sapien
P49129 cricetulus
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O62261 mus musculu
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PIR; A28067; A28067
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MGD; MGI:96745; Lamp1.
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P14562; P97620;

01-JAN-1990 (Rel. 13, Created)

01-NOV-1990 (Rel. 13, Last sequence update)

01-NOV-1997 (Rel. 35, Last annotation update)

Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1)

kDa lysosomal membrane glycoprotein) (LGP-120) (CD107A)

LAMP1 OR LAMP-1.
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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"Derived protein sequence, oligosaccharides, and membrane insertion of the 120-kDa lysosomal membrane glycoprotein (1gp120): identification of a highly conserved family of lysosomal membrane glycoproteins."; proc. Natl. Acad. Sci. U.S. a of area.
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MEDLINE=89017240; PubMed=3174652;
Howe C.L., Granger B.L., Hull M.,
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMME outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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STRAIN=Bristol N2;
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mitted (JAN-1996) to the EMBL/
SIMILARITY: TO YEAST YKL100C.
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Skurnik M. Batsford S., Mertz A.K.H., Schiltz E., Toivanen P. Skurnik M. Batsford S., Mertz A.K.H., Schiltz E., Toivanen P. Withe putative arthritogenic cationic 19-kilodalton antigen of Yersinia enterocolitica is a urease beta-subunit."; Infect. Immun. 61.2498-2504(1993).

-i- CARALYTIC ACTIVITY: Urea + H(2)0 = CO(2) + 2 NH(3).

-i- COPACTOR: Binds 2 nikkel ions per subunit (By similarity).

-i- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).

-i- PTM: Lys-221 is carbamylatted. The carbamoyl group provides ligands for the two nickel ions (By similarity).

-i- SIMILARITY: BELONGS TO THE UREASE FAMILY.
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MEDLINE=94320783; PubMed=8045421;
de Koning-Ward T.F., Ward A.C., Robins-Browne
"Characterisation of the urease-encoding gene
enterocolitica.";
Gene 145:25-32(1994).
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Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Yersinia.
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EMBL; Z18865; CAA79316.1; -.
PIR; S36028; S36028.
HSSP; P18314; 1FWF.
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STRAIN=6471/76 / Serotype 0:3;
MEDLINE=93273501; PubMed=8500886;
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InterPro; IPRO06680; Amidohydro_1.
InterPro; IPR005847; Urease.
InterPro; IPR005848; UreaseA.
pfam; PF01979; Amidohydro_1; 1.
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(EC 3.5.1.5) (Urea ami
76.9%;
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(Urea amidohydrolase)
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RC STRAIN=CO-92 / Biovar Orientalis;

RX MEDLINE=21470413; PubMed=11586360;

RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

RA Prentice M.B., Sebathia M., James K.D., Churcher C., Mungall K.L.,

RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

RT "Genome sequence of Yersinia pestis, the causative agent of plague.";

RI Nature 413:523-527(2001).
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EMBL; AF095636; AAC78634.1; -.
EMBL; AJ414153; CAC92906.1; -.
EMBL; AE013727; AAM94814.1; ALT_INIT.
PIR; AC0325; AC0325.
HSSP; P18314; 1FWF.
InterPro; IPR006680; Amidohydro_1.
InterPro; IPR005847; Urease.
InterPro; IPR005848; UreaseA.
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SEQUENCE FROM N.A.

STRAIN=6/69M;

STRAIN=6/69M;

Schbbane F., Devalckenaere A., Simonet M.;

"Characterization of the urease locus from Yersinia pestis.";

Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)

UREC OR YPO2667 OR Y1239.
                                                                                                                                                                                                                                                                                STRAIN=KIM5 / Biovar Mediaevalis;
MEDLINE=22137863, PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.
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NCBI_TaxID=632;
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Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PF01979; Amidohydro_1; 1.
Pfam; PF00449; urease; 1.
PROSITE; PS00145; UREASE_2; 1.
PROSITE; PS001145; UREASE_1; 1.
PROSITE; PS001120; UREASE_1; 1.
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PROSITE; PS00145; UREASE 2; 1.
PROSITE; PS01120; UREASE 1; 1.
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01-OCT-1996
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Riot B., Berche P., Simonet
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Bacteria, Proteobacteria;
Enterobacteriaceae, Yersinia.
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MEDLINE=94071953; PubMed=8250933;

An S., Yang J., Xia M., Goetzl E.J.

"Cloning and expression of the EP2

prostaglandin E2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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P35408;
phorbol ester.";

J. Mol. Med. 74:333-336(1996).

J. Mol. Med. 74:333-336(1996).

J. Mol. Med. 74:333-336(1996).

THIS RECEPTOR FOR PROSTAGLANDIN E2 (PGE2). THE ALTHIS RECEPTOR IS MEDIATED BY G-S PROTEINS THAT STIMULADENYLARIE CYCLASE. HAS A RELAXING EFFECT ON SMOOTH MUDELAY AN IMPORTANT ROLE IN REGULATING RENAL HEMODYNAMIL INTESTINAL EPITHELIAL TRANSPORT, ADRENAL ALDOSTERONE INTESTINAL FUNCTION.

AND UTERINE FUNCTION.

SUBCELLULAR LOCATION: Integral membrane protein.

-I- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                   MEDLINE=97015877; PubMed=8862514; Mori K., Tanaka I., Kotani M., Miyaoka Sasaki Y., Nakagawa O., Ogawa Y., Usui Narumiya S., Nakao K.; "Gene expression of the human prostagla differential regulation in monocytoid a
                                                                                                                                                                                                                              pseudogenes.";
Genomics 35:182-188(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                  prostaglandin E2 receptor EP2 subtype.";
J. Biol. Chem. 269:11873-11877(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bastien
                                                                                                                                                                                                                                                                                                                  Biochem.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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g, functional expression, and characterization of the
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B., Stolz M., Bufflier
the prostaglandin EP4 ;
                                                                                                                                                                                                                                                                                                                      Res.
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                                                                                                                      human prostaglandin E receptor EP4 subtype: in monocytoid and lymphoid lineage cells by
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Pred. No. 22;
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Catarrhini;
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(Prostanoid
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i; Hominidae; Homo.
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receptor gene and
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                                                  (PGE2). THE ACTIVITY OF THAT STIMULATES ON SMOOTH MUSCLE. MAY NAL HEMODYNAMICS,
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   PERIPHERAL BLOOK
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Ichikawa
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ID UZIP DROME

STANDARD; PRT; 4
P10379; Q960B4; Q9W0W7;
AC P10379; Q960B4; Q9W0W7;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence up
DT 15-SEP-2003 (Rel. 42, Last annotation
DE Unzipped protein precursor (Zipper pro
GN UZIP OR ZIP OR CG3533.
CS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Hexapo
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InterPro; 1:...

Pfam; Pf00001; 7tm 1; 1.

PRINTS; PR00237; GPCRHDDOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

A PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

A PROSITE; PS0062; G_PROTEIN_RECEP_F1
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GO; GO:0004957; F:prostagilandin E receptor a
GO; GO:0007188; P:G-protein signaling, coupl
GO; GO:0006955; P:immune response; TAS.
GO; GO:0006955; GFCR_Rhodpsn.
DEGR. DEGRONO276; GFCR_Rhodpsn.
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RISINILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RISINILARITY.
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7 (POTENTIAL).
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EXTRACELLULAR
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CYTOPLASMIC (
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5 (POTENTIAL).
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N-LINKED (GLCNAC. . .)
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(See http://www.isb-sib.ch/announce/
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sequence update) annotation update) (Zipper protein).

488

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Hexapoda;

Insecta;

Pterygota;

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RX MEDILIPE-2019606; PubMed=10731132;
RX Adams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Barlon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlon R.C., Bascer E.G., Helt G., Walson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bhandari D., Belshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Belshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borkova D., Botchan A.E., Domes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kinmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Moshrefi A., Walssenn D.L.,
RA Merkulov G., Stapleton M., Stupeki M.P., Smith T.,
RA Merkulov G., Stapleton M., Skupeki M.P., Smith T.,
RA
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                                                                                                                                                                                                                                                                                                                                               MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Dryddale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.;
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Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
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                                  STRAIN=Berkeley; TISSUB=Embryo;
MEDLINE=22426066; PubMed=12537569;
Stappleton M., Carlson J.W., Brokstein P., Yu C
George R.A., Guarin H., Kronmiller B., Pacleb
George R.A., Rubin G.M.,
                                                                                                                                                                                 SEQUENCE FROM
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                                                                                                                                                                                                                                                                                         review
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me; Drosophila.
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                                      C., Ch
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                                                                             Champe M.
                                          Park S.,
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                                          Wan K.H.,
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CONFLICT
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Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002)
-!- FUNCTION: Required for normal axon patterning
-!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as zero. The same by non-profit institutions as zero. The same by and ic modified and this statement is not removed. Usage by and ic modified and this statement is not removed. Usage by and ic
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EMBL; AE003465;
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                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=90136715; PubMed=2693962;
Knapp B., Hundt E., Kuepper H.A.;
"A new blood stage antigen of Plasmodium
the erythrocyte surface.";
                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum.
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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  MEDIINE-98190013; PubMed-9521758; Krim H., Certa U., Dobeli H., Jakob P., Hol W.G.C "Crystal structure of fructose-1,6-bisphosphate human malaria parasite Plasmodium falciparum."; Biochemistry 37:4388-4396(1998).
                                                                                                                                     MEDLINE=90271928; PubMed=2190085; Knapp B., Hundt E., Kuepper H.A.; "Plasmodium falciparum aldolase: "Plasmodium falciparum aldolase: Mol. Biochem. Parasitol. 40:1-12(
                                                                                                                                                                                                                                                    the erythrocyte surface. Mol. Biochem. Parasitol.
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                                                                                                                                   Mol. Biochem.
                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tities requires a license agreement (S. send an email to license@isb-sib.ch).
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                                                                                                CRYSTALLOGRAPHY
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65; AAF47312.2; -
39; AAK93563.1; -
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UNZIPPED PROTEIN
EXTRACELLULAR (P
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                                                                                                                                     gene
(1990)
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1.2.13)
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ved. Usage by ar
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                                                                                                                                                            and localization.";
                                             aldol
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DR EMBL; M28881; AAA29473.1; -.

DR EMBL; A13461; CAAO1107.1; -.

DR EMBL; A13461; CAAO1107.1; -.

DR EMBL; A13461; CAAO1117.1; -.

DR PIR; A44942; A44942.

PR PJB; 1A4542; A44942.

PR PJB; 1A4542; A44942.

PR PJB; A46942; A14942.

DR PFO00741; B1000741; A1dolase I.

DR PFO0074; B1000741; B1001ASE CLASS I; 1.

DR PFO0D75; PS001128; A1dolase I; 1.

DR PFO0D76; PS001128; A1dolase I; 1.

DR PFO0D76; PS00118; A1dolase I.

PS00118; PS00118; A1dolase I.

DR PFO0D76; PS00118; A1dolase I.

DR PFO0D76; A1dolase I.

DR
This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
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    moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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EMBL outstation -
    RESULT 10
MX STREY

ID MX STREY

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Best Local S
Matches 6
                                                                                                                  PIR; B43715; B43715.

InterPro; IPR005877; Gpos_vSIRK.

InterPro; IPR001899; Gram_pos_anchor.

InterPro; IPR001899; LPXTG.

InterPro; IPR006192; LPXTG.

InterPro; IPR006192; LPXTG.

InterPro; IPR003145; M_repeat.

Pfam; PF00746; Gram_pos_anchor; 1.

Pfam; PF02370; M; 7.

Pfam; PF02370; M; 7.

PFANTS; PR000115; GPSANCHOR:

ITGRPAMS; TIGR01167; LPXTG anchor; 1.

PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
       Antigen;
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VIRULENCE FACTOR-RELATED REMOVED BY SORTASE (POTEN 2 X REPEATS, TYPE A. A-1.

(POTENTIAL).

M PROTEIN

3; 1. Peptidoglycan-anchor; Repeat;

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MX_STRPY STANDARD;
p16946;
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01-AUG-1990 (Rel. 15, Last s
28-FEB-2003 (Rel. 41, Last a
Virulence factor-related M p
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                        EMBL; M23689; AAA26919.1; -.
EMBL; M31790; AAA26875.1; -.
PIR; B43715; B43715.
                                                                                                                                                                                                                                                                                                                               Streptococcus.
NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                            MEDLINE=90078078; PubMed=2687231;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-Serotype M49;
                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 GENAGASLY 363
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                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
annotation update)
protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 28; DB;
; Pred. No. 43;
1; Mismatches
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RESULT 11
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ID SELA HELPY
AC 026073
DT 16-0071
DT 28-FEBE
DE L-Sery
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16-0CT-2001
28-FEB-2003
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MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Telsischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougharty B.A.

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

MCKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,

Venter J.C.;
                                                                                       the European Bioinformatics Institute. They use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          UCA) during selenoprotein biosynthesis (By similarity).

-!- CATALYTIC ACTIVITY: L-sery)-tRNA(Sec) + selenophosphate selenocysteinyl-tRNA(Sec) + H(2)O + phosphate.

-!- COFACTOR: Pyridoxal phosphate (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: BELONGS TO THE SELA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                     pylori.";
Nature 388:539-547(1997).

-i- FUNCTION: Converts seryl-tRNA(Sec UCA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
L-seryl-tRNA(Sec) selenium transferase (EC 2.9.1.1) (Cysteinyl-tRNA(Sec) selenium transferase) (Selenocysteine synthase)
(Selenocysteinyl-tRNA(Sec) synthase).
SELA OR HP1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
    EMBL; AE000649; AAD08554.1; PIR; A64709; A64709. TIGR; HP1513; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori (Campylobacter
Bacteria; Proteobacteria; Epsilonp
                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of the gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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75.0%;
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3 X REPEATS, 7
C-1.
C-2.
C-3.
GLY/PRO-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLY/PRO-RICH (CELL WALL-SPANNING).
LPXTG SORTING SIGNAL (POTENTIAL).
AMIDE-LINKED TO CELL WALL (POTENTIAL);
4AD6D5A72F637839 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28; DB 1;
Pred. No. 43;
); Mismatches
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3 X
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                                                                                                                    http://www.isb-sib
                                                                                                                                       Usage
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MBL outstation -
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Best Local S
Matches 5
HUMAN STANDARD; PRT; 390 AA.

RBM9 HUMAN STANDARD; PRT; 390 AA.

C 043251; Q8TD00; Q8WYB1; Q96DZ6; Q96NL7; Q9UGW4;

T 16-OCT-2001 (Rel. 40, Created)

T 15-SEP-2003 (Rel. 42, Last sequence update)

J 15-SEP-2003 (Rel. 42, Last annotation update)

RNA-binding protein 9 (RNA binding motif proteir

RNA-binding protein 9 (RNA binding motif proteir

(Hexaribonuclectide binding protein 2) (Represso
                                                                                                                                                                                                                            Query Match
Best Local S
Matches
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InterPro; TPR004534; SelA.
Pfam; PF03841; SelA; 1.
Transferase; Pyridoxal phosphate; Selenium; Complete proteome.
Transferase; Pyridoxal phosphate; Selenium; Complete proteome.
BINDING 221 PYRIDOXAL PHOSPHATE (BY SIMILARITY)
386 AA; 43995 MW; BAC3DE6B50F3E859 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECOLI
KSS5 ECO
P42218;
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01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                EMBL; X74567; CAA52659.1; -.
PIR; 836653; 836653.
Pfam; PF05159; Capsule_synth; 1.
Polysaccharide transport; Transport.
Polysaccharide transport; 73058122C28027DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular analysis of region 1 of the Escherichia gene cluster: a region encoding proteins involved i expression of capsular polysaccharide.";
J. Bacteriol. 175:5978-5983(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
Enterobacteriaceae; Esche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roberts I.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pazzani C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93388530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88530; PubMed=8397187;
Rosenow C., Boulnois G.J.,
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Escherichia.
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75.0%;
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Pred. No. 45;
2; Mismatches
                                                                                                                                                                                                                            Score 28; DB
Pred. No. 45;
1; Mismatches
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RX MEDLINES 2005/165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeidd J.P., Babbage A.K.,
RA Elang M., Smink L.J., Ainscough R., Almeidd J.P., Babbage A.K.,
RA Barguley C., Bailey J., Barlow K.F., Bates K.N., Beagley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burges J.,
RA Conroy D., Corby N.R., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hall R.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mclay J., Mclaren S., McMurray A.A., Milne S.A., Morrimore B.J.,
Coell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.,
RA Hilligs S.H., Plumb R.M., Ramsay H., Ramsey Y., Rogers J.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Wijsht C.L., Hubbard T., Bertley D.R., Seck S., Rogers J., Shimizu N.,
RA Williams L., Williamson H., Wilner T.E., Wilming L.,
RA Wijsht C.L., Hubbard T., Bertley D.R., Seck S., Rogers J., Shimizu N.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Wight C.L., Hubbard T., Koshizaki Y., Aoki N., Mitsuyama S.,
RA Wight C.J., Wang Z., White J., Ran D., Shimizu N.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Misuyan D., Song L.,
RA Wight C.J., Wang Z., White J., Ran D., Shon D., Song L.,
RA Wight C.J., Wang Z., White J., Williamson D., Wu H., Yao Z.,
RA Wang O., Wang Y., Wang S., Marray J., Maller N., Minx P.,
RA Wang O., Wang Y., Wang S., Wohldmann P., Pepin K., Nelson R.,
RA Kim U.J., Shiker C., Wansley A., Wohldmann P., Pepin K., Nelson R.,
RA Kott I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
RA Kim S., Shakh T., Kanbashi H., Saite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE FROM N.A. (ISOFORM 1).

SIDUENCE FROM N.A. (Manda K., Kondo H., Yokoi T., Kodaira H., Nihomiya K., Wagatsuma M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Sato K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Watehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B. Sizuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., "NEDO human CDMA sequencing project.";

"NEDO human CDMA sequencing project.";

"NEDO human CDMA sequencing project.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collins J.E., Burton Submitted (NOV-1997)
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MEDILINE=21864496; PubMed=11875103;
NORTIS J.D. Fan D. Sherk A. McDonnell
"A negative coregulator for the human ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W.,
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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Isogai T.;
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Query Matcl
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Wilkinson P., Bodenteich
Tilahun Y., Wright H.;
"The DNA sequence of huma
Nature 402:489-495(1999).
                                                                                                                                                                                                         PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP 1
RNA-binding; Alternative sp
DOMAIN 121 197
DOMAIN 273 377
VARSPLIC 1 18
                                                                                                                                                                                                                                                                                                                                 EMBL;
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                    CONFLICT
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Pfam; PF00076; rrm; 1.
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Strausberg R.;
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                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                Genew; HGNC:9906; RBM9
InterPro; IPR000504; RI
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                                                                                                                                                     VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Interacts with ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                              L; AY072786; AAL67150.1; -.

(; AF239058; AAL71905.1; -.

L; AL003266; CAAL5842.1; -.

L; AK055213; BAB70875.1; ALT INIT.

L; AL079295; -; NOT ANNOTATED CDS.

L; AL049748; -; NOT_ANNOTATED_CDS.

L; BC013115; AAH13115.1; -.

L; BC013281; AAH25281.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note=No experimental SIMILARITY: Contains 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=4;
IsoId=043251-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=043251-3;
Note=No experim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=043251-2;
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Bodenteich
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 71.8%;
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ig protein that seems to act as a
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splicing.
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                      MV;
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SLPLV -> I (in isofo
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                                                                                               /FTIG-VSP_007182.

VYQDGEYGADLYGGYAAYKYAQPATATAATAAAAAAAAXSD
GYGRVYTADEYHALAEASYGVGAVASLYRGGYSREAPY
-> DWQPTDWHSLLLQPQPPLLQELQPLTVTVWAGCTQPTP
TWPLPLAMELALWRVYTEVATADLPPTEVT (in
 Score
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ALA-RICH.
                                                                            isoform 4
/FTId=VSP
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                               FTId=VSP_007183.
-> TQ (IN REF. 3).
-> F (IN REF. 4).
-> V (IN REF. 6; AAH13115)
-> G (IN REF. 4).
                       40D6C8C40764B317 CRC64;
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Matches
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InterPro; IPRO02000; Lamp.
Pfam; PF01299; Lamp; 1.
PRINTS; PR00336; LYSASSOCTDMP.
PROSITE; PS00310; LAMP_1; 2.
PROSITE; PS00311; LAMP_2; 1.
                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
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CHAIN 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane glycoproteins.
Cell. Mol. Biol. Res. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97021428; PubMed=8867788;
Uthayakumar S., Granger B.L.;
"Cell surface accumulation of overexpressed hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cricetulus griseus (Chinese hamster)
Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Rodentia; Sciuro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p49129; (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Upsosome-associated membrane glycoprotein 1 p
(Lysosomal membrane glycoprotein A) (LGP A).
LAMP1 OR LGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I. MOI. Biol. Res. 41:405-420(1995).
FUNCTION: PRESENTS CARBOHYDRATE LICANDS TO SELECTINS. ALSO
IMPLICATED IN TUNCE CELL METASTASIS (BY SIMILARITY).
SUBCELLULAR LOCATION: Type I membrane protein. Lysosomal.
THIS PROTEIN SHUTTLES BETWEEN LYSOSOMES, ENDOSOMES, AND THE
MEMBRANE (BY SIMILARITY).
DEPM: O- AND N-GLYCOSYLATED; SOME OF THE N-GLYCANS ATTACHED
LAMP-1 ARE POLYLACTOSAMINOGLYCANS (BY SIMILARITY).
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BY SIMILARITY.
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FIRST LUMENAL DOMAIN.
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DT 01-FBB-1995
DT 15-JUL-1998
DT 15-JUL-1998
DT 18-DEST
ON BACTERIA SUB-
ON BACTILLS SUB-
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ON BACTERIA SUB-
ON BACTERIA SUB-
RA HAGA K. Liu
RT "Sequence FRO)
RC STRAIN=168;
RA HAGA K. Liu
RT "Sequence FRO)
RC STRAIN=168;
RA HAGA K. Liu
RT "Sequence FRO)
RD SEQUENCE FRO)
RA BOTTISS R. ;
I [2]
RA BOTTISS R. ;
RA Ghim S.Y. G
RA Ghiseppi G. ;
RA Ghim S.Y. G
RA Ghiseppi G. ;
RA Ghiseppi G. ;
RA Ghiseppi G. ;
RA Ghim S.Y. G
RA GANONE D. O
RA FRICTO V. PO
RA NOONE D. O
RA NOONE D. O
RA RA SECONI A. ;
RA SECONIA A. ;
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RA KUISH F., OGASAWARA N., MOSZEY I., Albertini A.M., Borchert S.,
RA AZEVEGO V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA AZEVEGO V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouilser S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Guiseppi G., Cotter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Moone D., O'Railly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Sekiguchi J., Seanlan E., Schleich S., Schoes M., Sadaie Y.,
RA Sekiguchi A., Taconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
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"Sequence analysis of the 70kb
Bacillus subtilis chromosome,";
Submitted (JUL-1997) to the EME
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REMBL; BG9750; D69750.

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RMEDLINE=95270606; PubMed=7751298;

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4: sp_human:*

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11: sp_rodent:*

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08dvx3 streptococc
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P72591 synechocyst
09pky0 chlamydia m
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ALIGNMENTS

SUL 493	PRELIMINARY; PRT; 333 AA.
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YFMD protei	
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Bacteria;	Firmicutes; Bacillales; Bacillaceae; Bacillus.
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	DM N.A.
STRAIN=16	
	PubMed=9384377;
Kunst F.,	ra N., Moszer I., Albertini A.M., Alloni G.,
۲.	M.G., Bessieres P., Bolotin A., Borchert
BOTTISS K.	b., Brans A., Braum M., Brighett
RA Choi S.K., (Codani J.J., Connerton I.F., Cummings N.J., Daniel R.
Deniz	M., Dusterhoft A., Ehrlich S.D., E
Entian K.D	Errington J., Fabret C., Ferrari E.,
Fritz C.,	jita M., Fujita Y., Fuma S., Galizzi A
Ghim S.Y.,	Goffeau A., Golightly E.J., Grandi
Guiseppi G	, Haga K., Haiech J., Harwo
	ppel S., Hosono S., Hullo M.F., Itaya M.
Joris B.,	mata D., Kasahara Y., Klaerr-Blanchard
Kobayashi	ter P., Koningstein G., Krogh S., Kumano
Kurita K.,	idus A., Lardinois S., Lauber J., Lazarevic
Lee S.M., I	., Liu H., Masuda S., Mauel C., Medigue
Medina N.,	R.P., Mizuno M., Moesti D., Nakai S., Nobe
RA Noone D., C	Oudega B., Park
Parro V.,	., Portetelle D., Porwollik S., Presco
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RA Rieger M.,	volta C., Rocha E., Roche B., Rose
Sato T.,	E., Schleich S., Schroeter R., Scoffone F.,
. Sekiguchi	cowska A., Seror S.J., Serror P.,

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RP SECIES-S.aureus (strain Mu50), and S.aureus.

RC SPECIES-S.aureus (strain Mu50), and S.aureus.

RX MEDLINE-21311952; PubMed=11418146;

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

RA Migutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Migutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Migutani-Ui Y., Takahashi N.K., Sawano T., Yabuzaki J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
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Best Local S
Matches
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Submitted
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Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.;
"Cloning and sequencing of a 35.7 kb in the 70 degree 73 degree region of the Bacillus subtilis genome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and general stress response protein.";
Gene 194:191-199(1997).
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Nature 390:249-256(1997).
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01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2002 (TrEMBLrel. 20,
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Pfam; PF01032; FecCD; 1.
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                                                                                                                                                                                                                                                                                    SPECIES=S.aureus; STRAIN=SA502A; MEDILINE=97342847; PubMed=9197262; Ji G., Beavis R., Novick R.P.; "Bacterial interference caused by Science 276:2027-2030(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGRD (AGRD protein).
AGRD OR SAV2037 OR SA1842.1 OR SAS066
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Bacteria, Firmicutes, Bacillales, Staphylococcus
MCBI_TaxID=158878, 158879, 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus (strain Mu50 / Staphylococcus aureus (strain N315),
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8; Conserv
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the EMBL/GenBank/DDBJ
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Last annotation
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Pred. No. 3.4;
0; Mismatches
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Lancet 357:1225-1240(2001).
EMBL, AF001782; AAB63265.1; -
EMBL; AP003364; BAB58149.1; -
EMBL; AP003135; BAB43124.1; -
Complete proteome.
SEQUENCE 47 AA; 5149 MW;
                                                                                           01-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-MAR-2003 (TrEMBLrel. 23, L
Similar to lysosomal membrane
Mus musculus (Mouse)
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Q8XHH9;
Q1-MAR-2002
01-MAR-2002
01-MAR-2003
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Q922T9;
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical CPE2505.
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Hypothetical protein; Complete proteome.

SEQUENCE 463 AA; 51100 NW; 6EE3E385633DEEB9
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EMBL, AP003194; BAB82211.1; -.
InterPro, IPR002528; MatE.
Pfam; PF01554; MatE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium perfringens.
Bacteria; Firmicutes; Clostridia;
  Strausberg R. Strausberg R. Submitted (ARR-2001) to the EMBL; BC006785; AAH06785.1; InterPro; IPR002000; Lamp.
                                                                                                                                                                                                                                                                                                                                                                                             Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anae
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=13 / Type A; pubMed=11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium
                                           SEQUENCE FROM N
                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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6; Conserve
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                                                                            Chordata;
Rodentia;
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PRINTS; PR00336; LYSASSOCTDMP.
PROSITE; PS00310; LAMP 1; 1.
PROSITE; PS00311; LAMP 2; 1.
NON TER 1 1
SEQUENCE 189 AA; 20456 MW;
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01-MAR-2003
01-MAR-2003
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01-MAR-2003 (TrEMBLrel 23, Last sequence update)
01-MAR-2003 (TrEMBLrel 23, Last annotation update)
Conserved hypothetical protein, putative membrane SMU.337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Daub J., Mudge J., Blaxter M.L.;
"The mitochondrial genome of the nematode parasite Brug
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AF539716; AAN17809.1; -.
                                                                                   STRAIN=UA159 / ATCC 700610 / Serotype C;

MEDLINE=22295063; PubMed=12397186;

Ajdic D., McShan M.M., McLaughlin R.E., Savic G., Chang J.,

Addic D., McShan M.M., Tian R., Kenton S., Jia H., Lin S.,

Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S.,

Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti

"Genome sequence of Streptococcus mutans UA159, a cariogenic of
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SEQUENCE 259
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NCBI_TaxID=6279;
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Natl. Acad. Sci. U.S.A. AE014881; AAN58096.1; -
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(C STRAIN=CS7BL/6J; TISSUB=Lung;

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(X Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

(A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

(A Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,

(A Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

(A Arakawa T., Gojobori T., Bono H., Kasukawa T., Saito R.,

(A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

(A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

(A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

(A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,

(A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

(A Blake J., Boffelli D., Bojunga N., Carninoi P., de Bonaldo M.F.,

(A Blake J., Boffelli D., Bojunga N., Carninoi P., de Bonaldo M.F.,
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Submitted (DEC-2001) to t
EMBL; AY069968; AAL58070.
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Mammalia; Eutheria;
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PROSITE; PS00310; LAMP 1; 2.
PROSITE; PS00311; LAMP 2; 1.
SEQUENCE 406 AA; 43879 MW;
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Pred. No. 39;
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RESULT
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Best Local S
Matches 7
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Best Local S
Matches 6
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InterPro; IPR002000; Lamp.
Pfam; PF0129; Lamp; 1.
PRINTS; PR00316; LYGASSOCTDMP.
PROSITE; PS00310; LAMP_1; 2.
PROSITE; PS00311; LAMP_2; 1.
SEQUENCE 407 AA; 43936 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y., "Punctional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                          Q9M838;
Q9M838;
01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN_RECEP_F1 1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Bonck S.L., Castleberry T.A., Lu B., Owen T.A.;
"Pan troglodytes prostaglandin E2 subtype EP4 receptor.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY052641; AAL15039.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
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01-DEC-2001 (TrEMBLrel. 2), Last sequence update)
01-MAR-2003 (TrEMBLrel. 2), Last annotation update)
Prostaglandin E2 subtype EP4 receptor.
Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta;
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                                                                   T27C4.14 protein.
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) (TrEMBLrel. 15,
2 (TrEMBLrel. 21,
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87.5%;
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Last sequence update)
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2; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB
Pred. No. 74;
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BB
  Embryophyta; Tracheophyta;
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RESULT 11
Q98K8
ID Q98K8
AC Q08K8
AC Q98K8
AC Q08K8
AC Q98K8
AC Q08K8
AC Q98K8
AC Q9
RESULT 12
P72591
ID P7259
AC P7259
DT 01-FE
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DT 01-FE
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Best Local S
Matches 7
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Best Local S
Matches 6
P72591;
01-FEB-1997
01-FEB-1997
01-JUN-2002
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STRAIN-cv. Columbia;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.
Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC T27C4 genomic sequence.";
Submitteed (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC02288; AAF63780.1;
InterPro; IPR004314; DUF239.
Pfam; PF03080; DUF239; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
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01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation updat
0xidoreductase of short-chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 279 AA;
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EMBL, AP002997; BAB48933.1; -.
InterPro, IPR002198; ADH short.
Pfam; PF00106; adh short; 1.
PRINTS; PR00080; SDRFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome structure of Mesorhizobium loti.";
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(TrEMBLrel. 02, (TrEMBLrel. 02, CTEMBLrel. 21,
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                                                                                                                                                 PRELIMINARY;
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87.5%;
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Pred. No. 2e+0
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB
Pred. No. 69;
0; Mismatches
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STRAIN-MOPN / Nigg;

MEDLINE-20150255; PubMed=10684935;

Read T.D., Brunham R.C., Shen C., Gill S.R., H
white O., Hickey E.K., Peterson J., Utterback
Linher K., Weidman J., Khouri H., Craven B., B
Gwinn M., Nelson W., DeBoy R., Kolonay J., MCC
Elsen J., Fraser C.M.;
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                      "Genome sequences of Chlamydia trachomatis pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
EMBL; AE002301; AAF73547.1;
TIGR; TC0330;
                                                                                                                                                                                                                      InterPro; IPR001712; Bact_FHIPEP Pfam; PF00771; FHIPEP; 1. PR10175; PR00949; TYPE3IMAPROT.
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NCBI_TaxID=83560;
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ProDom; PD001557; FecCD; 1.
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                                                                                                                                                                                     Complete proteome. SEQUENCE 578 AA;
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                                                                                                                                                                                  Anabaena sp. (strain PCC /120/.
Plasmid pCC7120delta.
Bacteria; Cyanobacteria; Nostocales;
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MEDLINE-98325267; PubMed-9657932;
Bourgoin F., Guedon G., Gintz B.,
"Characterization of a novel insestreptococcus thermophilus.";
Plasmid 40:44-49(1998).
                                     EMBL; AP003604; BAB77421.1; -. Plasmid; Complete proteome. SEQUENCE 188 AA; 21357 MW;
                                                                 "Complete genomic sequence of cyanobacterium Anabaena sp. st CNAN Res. 8:205-213(2001).
                                                                                              MEDLINE=21595285; PubMed=11759840; Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Watanabe A., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;
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Bacteria; Firmicutes; Lactobacillales;
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US-08-252-991A-25625

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              Sequence 5, Appli
Sequence 3, Appli
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US-09-339-511-5
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Best Local
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27 69.2 447 4 US-09-252-991A-20563 27 69.2 448 4 US-09-194-452A-793 27 69.2 488 4 US-09-134-001C-4246 27 69.2 501 1 US-08-499-2154-4 27 69.2 597 1 US-08-462-184A-1 27 69.2 597 1 US-08-461-881B-1 27 69.2 597 1 US-08-461-881B-3 27 69.2 605 2 US-09-23-901A-23789 27 69.2 606 4 US-09-252-991A-23789 28 08 08 08-462-497B-2301 29 69.2 1544 US-09-252-991A-23789 20 66.7 35 4 US-09-31-311-3 26 66.7 35 4 US-09-31-218-436	45	44	43	42	41	40	3 9	ა 8	37	36	S	34	33	32	31	30	29
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ALIGNMENTS

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Sequence 5, Application US/09339511

Patent No. 6337385

GENERAL INFORMATION:

APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Patricia
APPLICANT: No. 6337385ick, Richard P.
APPLICANT: No. 6337385ick, Richard P.
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLCCOCCUS P.
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT APPLICATION NUMBER: 06/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOPTWAREN OF SEQ ID NOS: 8
SOPTWARENCE SECTIONS: 1998-06-24
RESULT 2
US-09-339-511-1
INSEQUENCE 1, Application US/09339511
Sequence 1, Application US/09339511
Sequence 1, Application Sequence 1, Applicant No. 6337385
APPLICANT: Mayville, Patricia APPLICANT: No. 6337385ick, Richard APPLICANT: No. 6337385ick, Richard APPLICANT: Ji, Guangyong
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOPTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence
PEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
OTHER INFORMATION: peptide
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position
US-09-339-511-5
                                                                                                                                                                                                                                                                                                                                                                    9; Conserv
  Muir, Tom
Mayville, Patricia
No. 6337385ick, Richard F
Beavis, Ronald
Ji, Guangyong
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                                                                                                                                                                                                                                                                                                                                                                      94.9%; Score 37; DB
100.0%; Pred. No. 2:
tive 0; Mismatches
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Query Match
Best Local Similarity
Thes 7; Conserve
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                                                                                                                                                                                                                                                             RESULT 4
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CURRENT FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 3
                                                                                                                                   GENERAL INFORMATION:
APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE
FILE REFERENCE: 63753/7
                                                    CURRENT APPLICATION NUMBER: US/08/861,476C
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08861476C
Patent No. 6447786
                                                                                                                                                                                                         Sequence 6, Application US/08861476C Patent No. 6447786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -08-861-476C-3
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CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 199-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.0
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LENGTH: 47
TYPE: PRT
ORGANISM: Staphylococcus aureus
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TITLE OF INVENTION:
TILE REFERENCE: 600
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Pred. No.
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Pred. No. 2.5e+05
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2.5e+05;
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US-08-861-476C-6
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                              NUMBER OF SEQ 1
SOFTWARE: Pate
SEQ ID NO 2
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                              Sequence 2, Application US/09339511 Patent No. 6337385 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILLING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 198-06-24
NUMBER OF SEO ID NOS: 8
NUMBER OF SEO ID NOS: 8
NUMBER OF SEO ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
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APPLICANT:
APPLICANT:
                                                               CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILLING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                             APPLICANT: Beavis, Ronald
APPLICANT: J1, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
                                                                                                                                                                                               APPLICANT:
LENGTH:
TYPE: PR
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OTHER INFORMATION: Xaa represents any amino acid at this position
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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o, 6337385
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7; Conservative
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No. 6337385ick, Richard
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Mayville, Patricia
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77.8%;
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Pred. No.
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2; Mismatches
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US-09-107-532A-4904
US-09-107-532A-4904
; Sequence 4904, Application US/09107532A
; Sequence 4904, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; GENERAL INFORMATION: DOUGETTE-Stamm
; HOUSE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
ENTEROCOCCUS
                                                                                           ; NAME/KEY: misc feature; LOCATION: (B) LOCATION 1...339; SEQUENCE DESCRIPTION: SEQ ID NO: 4904: US-09-107-532A-4904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
, LOCATION: (5)
, OTHER INFORMATION: Xaa represents any amino US-09-339-511-2
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Query Match
Best Local Similarity 75.0
Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                            TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4904:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION UNDMER: 60/081571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                          LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GANAXSSLF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVNAXASLF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Waltham
                                                                                                                                                                                           ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description of Artificial Sequence: Synthetic peptide
                                          76.9%;
75.0%;
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Pred. No. 2.5e
1; Mismatches
                         Score 30; DB 4;
Pred. No. 43;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
2.5e+05;
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                                                              Length 339;
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RESULT 10
US-09-339-511-7
J Sequence 7, Application US/09339511
Patent NO. 6337385
GENERAL INFORMATION:
APPLICANT: Muir, Tom
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US-09-252-991A-28048
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US-09-252-991A-27559
                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT ETILING DATE: 199-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 198-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27559

LENGTH: 464

TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 28048
LENGTH: 464
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Marc J.
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Best Local
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                                                                                                                                                                                                                                                                                    Query Match
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR:FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                               Similarity 66. 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09252991A
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Pred. No. 62;
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                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                        4.
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US-08-115-365-2
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US-09-882-835-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
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                                                             Patent No. 5605814
GENERAL INFORMATION:
APPLICANT: ABRAMO'
APPLICANT: ADAM, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version SEQ ID NO 2
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Patent No. 6462187
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATELLY OF STATE OF SECULATION OF SECULAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/882,835
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/211,673
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa represents any amino acid at this position
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LICANT: Bandaru, Rajasekhar
LE OF INVENTION: 22109, A NOVEL HUMAN THIOREDOXIN FAMILY
LE OF INVENTION: MEMBER AND USES THEREOF
E REFERENCE: 10448-063001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                             197 GVNSYPSLF 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>..</u>.
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No. 6337385ick, Richard
Beavis, Ronald
                                                                                                                                                                                                   Application US/08115365
                                ABRAMOVITZ, MARK
ADAM, MOHAMMED
BASTIEN, LISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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GRYGORCZYK, RICHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guangyon
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77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 332;
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US-08-115-365-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 1906
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 6
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/115,365
FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                              SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIF: 0,700
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BC PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: WALLEN III, JOHN W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN WALLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SAWYER, NICOLE TITLE OF INVENTION: DNA EI NUMBER OF SEQUENCES: 2
SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586,89
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-DOS/M9-DOS
OPERATING SYSTEM: PC-DOS/M9-DOS
                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  APPLICANT: SAWYER, NICOLE TITLE OF INVENTION: DNA E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: J
STREET: P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 75.0
                                                                                                                                                          CITY: RAHWAY
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                            ADDRESSEE: JOHN WALLEN STREET: P.O. BOX 2000,
                                                                                                                          COUNTRY: UZIP: 07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRATION NUMBER:
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GRYGORCZYK, RICHARD
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RUSHMORE, THOMAS H.
                                                                                                                                                                                                                                                                                                                         METTERS, KATHLEEN
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75.0%;
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                                                                                                                                                                                                                                                                                                      THOMAS H.
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   US/08/586,897
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Pred. No.
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RESULT 15
US-09-252-991A-25625
; Sequence 25625, Application US/09252991A
; Patent No. 6551795
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US-09-339-511-4
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NAME: WALLEN III, JOHN W.

REGISTRATION NUMBER: 35,403

REFERENCE/DOCKET NUMBER: 19066

TELEPHONE: 908-594-3905

INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                     Query Match 71.8%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: No. 6337385ick, Richard P.
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
TITLE OF INVENTION: INTERFERENCE
TITLE REPERENCE: 600-1-231N
                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position:
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 9
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STRANDEDNESS: single
TOPOLOGY: linear
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Similarity 75.0%;
6; Conservative
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                                                                                                                                                                                     Score 28; DB 4;
Pred. No. 2.5e+05;
1; Mismatches (
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GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

FILE REFERENCE: 107196.136

FULLE REFERENCE: 107196.136

CURRENT PRILICATION NUMBER: US/09/252,991A

CURRENT PRILICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILLING DATE: 1999-02-18

PRIOR FILLING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25625

LENGTH: 205

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-25625

Query Match
Best Local Similarity 75.0%; Pred. NO. 69;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 CVNAXASI 8

| CVNAXASI 8
| CVNAXASI 8
| CVNAXASI 8
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| CVNAXASI 78
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Search completed: January 29, 2004, 15:03:22 Job time : 12.1176 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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18: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Match
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39
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Copyright (c) 1993 - 2004 Compugen Ltd.
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     BB
       US-10-032-950-5
US-10-031-944-3
US-10-201-444-3
US-10-201-444-6
US-10-201-444-6
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Sequence 1, Appli
Sequence 3, Appli
Sequence 6, Appli
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Sequence 11888, A
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Sequence 1638, Ap
Sequence 1638, Ap
Sequence 1698, Ap
Sequence 1, Appli
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7, Appli
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16 29 74.4 468 12 US-10-369-493-12194 Sequence 12194, A 17 29 74.4 488 12 US-10-295-561 Sequence 3, Appli 19 29 74.4 488 12 US-10-295-677A-296 Sequence 296, App 21 29 74.4 488 12 US-10-295-677A-296 Sequence 297, App 21 29 74.4 605 9 US-09-841-132-574 Sequence 297, App 22 29 74.4 747 10 US-09-978-595A-459 Sequence 459, App 23 29 74.4 747 10 US-09-978-95A-459 Sequence 459, App 25 29 74.4 747 10 US-09-978-189-459 Sequence 459, App 26 29 74.4 747 11 US-09-978-189-459 Sequence 459, App 27 29 74.4 747 11 US-09-978-189-459 Sequence 459, App 28 29 74.4 747 11 US-09-978-189-459 Sequence 459, App 29 29 74.4 747 11 US-09-978-189-459 Sequence 459, App 20 29 74.4 747 11 US-09-978-191A-459 Sequence 459, App 21 29 74.4 747 11 US-09-978-191A-459 Sequence 459, App 22 29 74.4 747 11 US-09-978-191A-459 Sequence 459, App 23 29 74.4 747 11 US-09-978-191A-459 Sequence 459, App 24 29 74.4 747 11 US-09-978-191A-459 Sequence 459, App 25 29 74.4 747 11 US-09-978-191A-459 Sequence 459, App 26 29 74.4 747 11 US-09-978-191A-459 Sequence 459, App 27 29 74.4 747 11 US-09-978-191A-459 Sequence 459, App 28 29 74.4 747 11 US-09-978-191A-459 Sequence 459, App 29 29 74.4 747 11 US-09-978-191A-459 Sequence 459, App 20 29 74.4 747 11 US-09-978-191A-459 Sequence 459, App 21 29 74.4 747 11 US-09-978-193A-459 Sequence 459, App 22 29 74.4 747 11 US-09-978-193A-459 Sequence 459, App 23 29 74.4 747 11 US-09-978-193A-459 Sequence 459, App 24 29 74.4 747 11 US-09-978-193A-459 Sequence 459, App 25 75 76 76 76 76 76 76 76 76 76 76 76 76 76
9 74.4 468 12 US-10-369-493-12194 Sequence 3.74.4 488 12 US-09-826-509-561 Sequence 3.74.4 488 12 US-09-826-509-561 Sequence 3.74.4 488 12 US-09-826-509-561 Sequence 3.74.4 488 12 US-09-826-5078-296 Sequence 2.74.4 488 12 US-09-978-2958-459 Sequence 2.74.4 605 9 US-09-978-2958-459 Sequence 4.74.7 10 US-09-978-2958-459 Sequence 4.74.7 10 US-09-978-2958-459 Sequence 4.74.7 10 US-09-978-2958-459 Sequence 4.74.7 11 US-09-978-2958-2959 Sequence 4.74.7 11 US-09-978-
4.4 468 12 US-10-369-493-12194 Sequence 3.4.4 488 12 US-10-320-351-3 Sequence 3.4.4 488 12 US-10-320-351-3 Sequence 3.4.4 488 12 US-10-295-027-1326 Sequence 3.4.4 488 12 US-10-295-027-1326 Sequence 3.4.4 488 15 US-10-225-567A-296 Sequence 2.9.4.4 488 15 US-10-225-567A-296 Sequence 2.9.4.4 747 10 US-09-978-295A-459 Sequence 4.9.4 747 10 US-09-978-192A-459 Sequence 4.9.4 747 10 US-09-978-192A-459 Sequence 4.9.4 747 11 US-09-978-192A-459 Sequence
86 12 US-10-369-493-12194 Sequence 3. 88 12 US-09-826-509-561 Sequence 3. 88 12 US-09-826-509-561 Sequence 3. 88 12 US-09-826-508-326 Sequence 3. 88 15 US-10-295-5678-296 Sequence 2. 89 US-09-841-32-574 Sequence 2. 89 US-09-841-32-574 Sequence 2. 89 US-09-978-295A-459 Sequence 3. 80 US-09-978-295A-459 Sequence 4. 80 US-09-978-192A-459 Sequence 4. 80 US-09-978-192A-459 Sequence 4. 81 US-09-978-192A-459 Sequence 4. 81 US-09-978-191A-459 Sequence 4. 81 US-09-978-191A-459 Sequence 4. 82 US-09-978-191A-459 Sequence 4. 83 US-09-978-191A-459 Sequence 4. 84 US-09-978-191A-459 Sequence 4. 85 US-09-978-191A-459 Sequence 4. 86 US-09-978-191A-459 Sequence 4. 87 US-09-978-191A-459 Sequence 4. 87 US-09-978-191A-459 Sequence 4. 88 US-09-978-191A-459 Sequence 4. 88 US-09-978-191A-459 Sequence 4. 88 US-09-978-191A-459 Sequence 4. 89 US-09-978-193A-459 Sequence 4. 80 US-09-978-193A-459 Sequence 4.
2 US-10-369-493-12194 Sequence 12 US-10-20-513 Sequence 12 US-10-25-507-1326 Sequence 23 US-10-25-5671 Sequence 23 US-10-25-5671 Sequence 23 US-10-25-5671 Sequence 23 US-10-25-5671 Sequence 24 US-10-25-5671 Sequence 25 US-10-25-78-697-459 Sequence 25 US-10-25-78-608A-459 Sequence 25 US-10-25-78-13-14-459 Sequence 25 US-10-25-78-13-14-459 Sequence 25 US-10-25-78-13-459 Sequence 25
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App 1 A App 2 App

ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: Mair. Tom
APPLICANT: Mayville, Patricia
APPLICANT: Mo. US20020077453A1ick, Richard F.
APPLICANT: No. US20020077453A1ick, Richard F.
APPLICANT: Ji, Guangyong
ITILE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
ITILE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOPTWARE: Patentin Ver. 2.0
                                                                                                                                                                  TYPE: PRT
ORGANIAM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
NAME/KEY: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position
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Best Local S
Matches 9
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                             GVNAXASLF
  GVNAXASLF
                                                                                      Conservative
                                           9
                                                                                 94.9%; Score 37; DB
100.0%; Pred. No. 7e-
tive 0; Mismatches
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                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/201,444
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US/08/861,476
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ'ID NOS: 8
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
                                                                       Query Match
Best Local S
Matches 7
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10201444 Publication No. US20030078378A1 GENERAL INFORMATION:
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APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453Alick, Richard
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CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REPERENCE: 63753/7
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TITLE OF INVENTION: NOTEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
                                                                                                                                                              TYPE: PRT ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                         LENGIH:
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8; Conserv
                                                                       Similarity 77. 7; Conservative
GVNACSSLF 9
                                  GVNAXASLF 9
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                                                                       84.6%; Score 33; DB 15;
77.8%; Pred. No. 7e+05;
cive 1; Mismatches 1
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Pred. No.
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RESULT 4 US-10-201-444-6

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; LENGTH: 47
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-6
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Best Local S
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APPLICANT: Castleberry
APPLICANT: Lu, Bihong
APPLICANT: Owen, Thoma
APPLICANT: Smock, Stev
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Publication No. US20030078378A1
GENERAL INFORMATION:
APPLICANT, New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE, 63753/7
                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                          Sequence 6, Application US/10032950 Publication No. US20020077453A1
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CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US/08/861,476
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Smock, Steven
TITLE OF INVENTION: DNA ENCODING THE CHIMPANZEE PROSTAGLANDIN E2 RECEPTOR EP4 SUBT
FILE REFERENCE: PC11827AGPR
CURRENT APPLICATION NUMBER: US/10/243,351
CURRENT FILING DATE: 2002-09-13
                                                                            APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453A1ick,
APPLICANT: Beavis, Ronald
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PRIOR APPLICATION NUMBER: US 60/322,915
PRIOR FILING DATE: 2001-09-17
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TYPE: PRT
PPLICANT: Ji, Guangyong
ITLE OF INVENTION: NOVEL STAPHYLOCOCCUS
ITLE OF INVENTION: INTERFERENCE
ILE REFERENCE: 600-1-231N
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Owen, Thomas A.
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                                                                                                  Richard P.
                                             PEPTIDES FOR BACTERIAL
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US-10-369-493-11888
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 11888
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                                                                                                                                                                                                                                                                                                               Sequence 14064, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: (Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: FLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
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OTHER INFORMATION: Xaa represents any amino acid at this position of the position 
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TYPE: PRT
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ORGANISM: Artificial Sequence
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Similarity 87.5%;
7; Conservative
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llarity 77.8%;
Conservative
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Pred. No. 7e+0
2; Mismatches
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Pred. No.
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US-10-032-950-2
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14064
LENGTH: 800
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                                                                                                                                                   Sequence 7334, Application US/09864408A Publication No. US20040009474A1 GENERAL INFORMATION:
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Best Local
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IIILE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERPERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: NO. US20040009474A1el Human
FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24
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APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453Alick, Richard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: VARIANT
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hes 7; Conserv
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77.8%;
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77.8%;
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Pred. No. 7e+05;
1; Mismatches
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Pred. No. 1.1e+02;
0; Mismatches 2
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                                                                                                 Polynucleotides and Polypeptides
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Best Local Similarity
Matches 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-292-798-1638
                                                                                                                                                                                                              Sequence 2252, Application US/10017161 Publication No. US20030143668A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1638
LENGTH: 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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APPLICANT: SUWA, MA
            APPLICANT: SUWA, MAKIKO
APPLICANT: ASIANA, VUTAKA
APPLICANT: AKIYANA, VUTAKA
APPLICANT: AKIYANA, VUTAKA
APPLICANT: ABURATANI, HIROVUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: UF 2001/246789
PRIOR APPLICATION NUMBER: UF 2001/246789
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: AKTYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANGSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
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SOFTWARE: FastSEQ for Windows
EQ ID NO 7334
NUMBER OF SEQ ID NOS: 2430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Wherein Kaa may be any naturally occuring amino acid
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CANT: ASAI, KIYOSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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o. US20030235833A1
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Pred. No. 94;
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; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-2252
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Publication No. US20030235833A1
GENERAL INFORMATION:
                                                                                                        SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/10032950 Publication No. US20020077453A1
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Best Local
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APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-16-18
NUMBER OF SEQ ID NOS: 2070
SOFTMARE: PATENTIN OFF: 2.1
                                                                                                                                                 CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                               APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Mayv
APPLICANT: No.
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FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                        ORGANISM: Artificial Sequence
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Local Similarity 66.7%;
les 6; Conservative
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No. US20020077453Alick, Richard P.
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Pred. No.
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Pred. No.
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Mismatches
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APPLICANT: Bandaru, Rajasekhar
APPLICANT: Kapeller-Libermann, Rosana
ITITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
ITITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
ITITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
FILE REFERENCE: 10440-188001
CURRENT APPLICATION NUMBER: US/10/145,586
CURRENT FILING DATE: 2002-05-14
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 95
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46
LENGTH: 332
TYPE: PRI
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 46, Application US/10145586
Publication No. US20030138890A1
GENERAL INFORMATION:
APPLICANT: Alexandra Glucksmann, Maria APPLICANT: Silos-Santiago, Inmaculada APPLICANT: M. Galvin, Katherine APPLICANT: Weich, Nadine
APPLICANT: Curtis, Rory A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-7
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Search completed: January 29, 2004, 15:01:46 Job time : 26.5441 secs
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US-10-145-586-46
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Best Local Similarity 66.7%;
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                                                                                    197 GVNSYPSLF 205
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                                                                                                                              1 GVNAXASLF 9
                                                                                                                                                                              6; Conservative
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
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10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
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21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
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23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
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ALIGNMENTS

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(MAYV/)
(NOVI/)
(BEAV/)
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24-JUN-1999;
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                    New cyclic peptides, infections ~
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MAYVILLE P.
NOVICK R P.
BEAVIS R.
JI G.
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                                                                Mayville P,
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99US-0339511.
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention. The present invention also describes a method for treating Staphylococcus aureus infection comprising the administration of a composition comprising (I). (I) has antibacterial activity, and can be used as an agr gene response inhibitor. The peptides are useful for treating S. aureus infections.
The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is a secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. Preferred peptides may have the sequence NH2-X(n)-z_xX(y)-COOH, with a cyclic bond between the Z residue and COOH other than a thioester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus antibacterial;
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                                                                                                  Claim 7;
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                                                                                                                                 Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
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                    This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
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Pred. No.
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9.3e+05;
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RESULT 6
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Best Local
                                                                                                                                                                      This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus infection; AgrD; agr response; treatment; virulence factor.
                            AAM50907 standard;
                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                         24-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus
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7; Conserv
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                                                                                                                 Similarity 7; Conser
                                                                            GVNASSSLF
                                                                                              GVNAXSALF
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NEW YORK STATE
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                            Peptide;
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                                                                                                                           89.7%;
77.8%;
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1; Mismatches
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                                                                                                              Score 35; DB 21;
Pred. No. 9.3e+05;
1; Mismatches 1;
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9.3e+05;
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AAM50907;

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(90:5:5) for 4 hr. The partially protected peptide-alpha carboxylates were then dissolved in DMF and treated with PyBOP and a catalytic amount of dimethylaminopyridine. Cyclization was complete after 2 hr. The remaining protecting groups were then removed by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the agr response of Staphylococcus aureus. The thiololactone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure with a lactone (as in the present case) or a lactam can destroy agr response activating activity while preserving and enhancing inhibitory activity. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus
                                                                                                                                                                                                                        The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AAM5089-906). The peptide corresponds to the Staphylococcus aureus AgrDII sequence with a Cys5 to Ser mutation (lactone). It was synthesised on a Wang-resin using an Fmoc N-alpha protection strategy. Following chain assembly, the peptide was cleaved from the support and the Ser-5 residue deprotected by treatment with a trilluoroacetic acid:anisole;water mixture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYRQ )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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UNIV NEW YORK STATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide used in cyclic peptide production
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infection; therapy; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                   cyclic AgrD-autoinducing peptide for bacterial for treating Staphylococcus aureus infection in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
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peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novick
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                                                                                                                                                                                                                                                                                                                                                           English
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Query Match Best Local

Similarity

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DB 23; 9.3e+05;

Length 9;

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GVNAXSALF

Query Match Best Local

Matches

Similarity 7; Conserv

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Score 35; DB Pred. No. 9.3e 1; Mismatches

DB 23; 9.3e+05;

Length 9; Indels

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RESULT 7
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                                                                                The present sequence is that of a novel synthetic AgrD2 linear thioseter peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylococus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrP3 containing a beta-lactamase reporter gene fused to the agrP3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. Unlike an AgrD2 response to be monitored spectrophotometrically. Unlike an AgrD2 response to be interactivate or inhibit the agr response, even when added to cultured cells at um concentrations. The invention provides claimed cyclic peptides (see AMM50099) of and methods for preparing them. The cyclic peptides are useful for infaction interference, especially for the treatment of S. aureus
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-170774/22.
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therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibacterial;
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RESULT 9
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fixed to the agr83 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone cyclic peptide (see AAM51001), the present peptide was unable to either activate or inhibit the agr response, even when added to cultured cells at uM concentrations. The invention provides claimed cyclic peptides (see AAM5999) gos and AAM5099) and methods for preparing them. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of a novel synthetic AgrD2 linear free acid peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis o virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the
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Pred. No. 9.3e+05;
1; Mismatches 1
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standard; Peptide;

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                                                                                                             The present sequence is that of a novel synthetic AgrD2 lactone cyclic peptide in which residue 5 of the peptide is derived from an AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrP3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. The lactone AgrD2 peptide inhibited the agr response of group I. I or III strains. The invention provides claimed cyclic peptides (see AnM50899-906 and AAM50999) and methods for preparing them, especially peptides where the cyclic bond is a lactam or lactone bond. The cyclic peptides are useful for bacterial interference, cepecially for the treatment of S. aureus infection.
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Best Local (
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Pred. No. 9.3e+05;
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Synergistic antibiotic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 33; 134pp; English
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07-DEC-2000; 2000US-254398P.
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                                                                                   S. aureus peptide #1 used for bacterial interference.
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                              Staphylococcus aureus infection; cyclic peptide; AgrD;
                                                                                                                                                                                                                                                            AAY67851 standard; peptide; 9 AA.
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(QUOR-) QUOREX PHARM INC.
(UYTE-) UNIV TECHNOLOGIES
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Pred. No. 9.3e+05
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  24-JUN-1999;
                                                                                         Misc-difference
                                                                                                                                                    Staphylococcus aureus infection; AgrD; agr response; treatment; virulence factor.
                                                                                                                                                                                        Staphylococcus aureus AgrDII derived peptide sequence
                                                                                                                                                                                                                   25-APR-2000
                                                                                                                                                                                                                                           AAY67861;
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                                                                             /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                               87.2%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB
Pred. No. 9.3e
1; Mismatches
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RESULT 13
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                                                                               (MUIR/) MUIR T W. (MAYVILLE P. (NOVI/) MOVICK R P. (BEAV/) BEAVIS R. (JIGG/) JI G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
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8; Conservative
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99US-0339511
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88.9%;
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                                                                           Claim 7;
                                                                                                                                                                                                                                                                      (UYRQ )
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                                                                                                                  subject
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interference and
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ting S. aureus infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVNAXSSLF
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infection; therapy; cyclic.
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peptide"
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The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of Staphylococcus aureus. It is an AgrD-autoinducing peptide, where

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RESULT 15
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                                                24-JUN-1998;
                                                                                           24-JUN-1999;
                                                                                                                                         08-JAN-2002
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infection; therapy; cyclic.
                                                98US-090402P
                                                                                              9908-0339511
                                                                                                                                                                                                                                     /note= "note linked to
    peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Ser(Bz1)"
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                                                                                                                                                                    acid (Dpr) mutation (lactam). It was synthesised on a Wang-resin Co using an Fmoc N-alpha protection strategy. Following chain assembly, the peptide was cleaved from the support and the Dpr-5 residue deprotected by treatment with a trifluoroacetic acid:anisole:water carboxylates were then dissolved in DMF and treated with PyBop.

CC Cyclization was complete after 2 hr. The remaining protecting groups were removed by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the agr response of Staphylococcus aureus. The thiololactone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure with a lactam (as in the present case) or a lactone can construct with a lactam (as in the present case or structure with a lactam (as in the present case or a structure with a lactam (as in the present case or a structure with a lactam (as in the present case or a structure with a lactam (as in the present case or a structure with a lactam (as in the present case or a structure with a lactam (as in the present case or a structure with a lactam (as in the present case or a structure with a lactam (as in the present case or a structure with a lactam (as in the present case or a section of the thiologically for the treatment of S. aureus
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Matches
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8; Conserv
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  Score 34; DB 23;
Pred. No. 9.3e+05;
1; Mismatches 0;
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Listing first 45 summaries
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39
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Matches Query Match

Local Similarity 66.

82.1%; Score 32; DB 66.7%; Pred. No. 13; vative 2; Mismatches

2; Length 382; Indels

0

Gaps

0

	RESULT 2 A28067 A28067 A28067 Lysosomal membrane glycoprotein LAMP-1 - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #t C;Accession: A28067 R;Chen, J, W, Cha, Y, Yuksel, K.U.; Gracy, R.W.; Aug J. Biol. Chem. 263, 8754-8758, 1988 A;Title: Isolation and sequencing of a cDNA clone end A;Title: Isolation and sequencing of a cDNA clone end A;Reference number: A28067; MUID:88243732; PMID:33791 A;Accession: A28067 A;Accession: A28067 A;Molecule type: mRNA A;Mo	Query Match B4.6%; Score 33; DB 2; Best Local Similarity 77.8%; Pred. No. 0.87; Matches 7; Conservative 1; Mismatches 1 Qy 1 GVNAXSALF 9 Db 24 GVNACSSLF 32	30 28 71.8 341 2 G89996 31 28 71.8 346 2 S56786 32 28 71.8 346 2 S56786 32 28 71.8 452 F64053 33 28 71.8 452 F64053 34 28 71.8 452 P93366 36 28 71.8 452 P93366 37 28 71.8 543 2 D93366 38 28 71.8 543 2 D93366 39 28 71.8 655 2 G89189 41 28 71.8 803 2 T39530 42 28 71.8 803 2 T39530 42 28 71.8 803 2 T39530 42 28 71.8 803 2 T39530 43 28 71.8 803 2 T39530 44 28 71.8 803 2 T39530 45 28 71.8 803 2 T39530 46 28 71.8 803 2 T39530 47 28 71.8 803 2 T39530 48 71.8 803 2 T39530 49 28 71.8 803 2 T39530 40 28 71.8 803 2 T39530 41 28 71.8 803 2 T39530 42 28 71.8 803 2 T39530 43 28 71.8 803 2 T39530 44 26 71.8 803 2 T39530 45 28 71.8 803 2 T39530 46 28 71.8 803 2 T39530 47 28 71.8 803 2 T39530 48 71.8 803 2 T39530 49 28 71.8 803 2 T39530 40 20 71.8 803 2 T39
1050th 300.	#text_change 20-Aug-1999 August, J.T. encoding lysosomal membrane glycopr. 79044 AA39411.1; PID:9293692 Pesidue 1 as Leu and CCG for residue	Length 47; ; Indels 0; Gaps 0;	hypothetical prote glycoprotein endop kpsD protein - Esc probable polysacch 4-chlorobenzoate-C DNA-binding protei NADH2 dehydrogenas cholesterol oxidas peptidase (M3 fami phosphotransferase protein 73276A.3 (hypothetical prote probable transcrip hypothetical prote sEC24 protein - ye genome polyprotein teaxt_change 22-Oct-2001 teaxt_change 22-Oct-2001 text_change 72-Oct-2001 thext_h; Kobayashi, I.; Cui, L.; Oc Inoue, R.; Kaito, C.; Sekimizu, K. H; Hiramatsu, K. H; Hiramatsu, K. B146 GSPDB:GN00149

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A;Molecule type: mRNA
A;Residues: 22-407 <HIM>
A;Residues: 22-407 <Pre>
F;22-407/Product: 1ysosomal membrane glycoprotein, 107K #status experimental 
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A;Residues: 1.407 <HOW>
A;Residues: 1.407 <HOW>
A;Cross-references: EMBL:J03672
A;Cross-references: EMBL:J03672
A;Note: the authors translated the codon GGG for residue 15 as R;Himeno, M.; Noguchi, Y.; Sasaki, H.; Tanaka, Y.; Furuno, K.; FEBS Lett. 244, 351-356, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Howe, C.L.; Granger, B.L.; Hull, M.; Green, S.A.; Gabel, C.A.; Helenius, A.; Mellman, Proc. Natl. Acad. Sci. U.S.A. 85, 7577-7581, 1988
A;Title: Derived protein sequence, oligosaccharides, and membrane insertion of the 120-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120K lysosomal membrane glycoprotein precursor N,Alternate names: sialoglycoprotein C,Species: Rattus norvegicus (Norway rat)
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 03-May-199
C;Accession: A60534
R;Heffernan, M.; Yousefi, S.; Dennis, J.W.
Cancer Res. 49, 6077-5084, 1989
A;Title: Molecular Molecular Station of P2B/LAMP-1, a major protein target A;Reference number: A60534, MUID:90002989; PMID:2676155
A;Accession: A60534
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A;Title: Isolation and sequencing of a cDNA clone encoding 107 kDa sialoglycoprotein in A;Reference number: S03331; MUID:89153580; PMID:2920835
A;Accession: S03331.
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A;Molecule type: mRNA
A;Residues: 1-405 <HEF>
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C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 03-May-1996
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2; Mismatches
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RESULT

alpha-mannosidase (EC C;Species: Emericella

3.2.1.24) nidulans,

Emericella nidulans
 Aspergillus nidulans

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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C;Accession: C69812 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Beri C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; (C.; Bron, S. D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, I.; Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino; A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Fark, S.H.; Parro, V.; Pohl, T.M.; Portete, R.; Geger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Saddie, Y.; Sato, T.; Scanid, A.; Authors: Schleich, S.; Schroeter, R.; Scoffene, F.; Sekiguchi, J.; Sekowska, A.; Seinethors: Yoshikawa, H.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyar, M.; Mitters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyar, M.; Dishikawa, H.; Zumstein, E.; Yoshikawa, H.; Vasumocto, K.; Yata, K.; Yoshida, A; Patthors: Yoshikawa, H.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; A; A; A; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         manganese transport protein all7601 [imported] - Nostoc sp. (strain PCC 7120) plasmid C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AF2539
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                                                                                                                                                                                                           A;Genome: plasmid
C;Superfamily: natural resistance-associated macrophage protein
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AF2539
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                                                                                                                                                                                                                                                                                                           C; Genetics
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A;Experimental source: strain PCC 7120
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GVSAASAIF 309
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C;Date: 22-Oct-
C;Accession: T3
R;Eades, C.J.;
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ferric exochelin uptake protein fxuC - Mycobacterium smegmatis (fragment)
C;Species: Mycobacterium smegmatis
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 22-Oct-19
C;Accession: S60885
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A;Title: Identification and analysis of a class 2 alpha-mannosidase
A;Reference number: Z20843; MUID:98119762; PMID:9451011
                                                  A; Map position:
                                                                A; Gene: CESP: F45H11.1
                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-298 <WIL>
                                                                                                                                                                                    submitted to the EMBL Data Library, A;Reference number: Z19537
A;Accession: T22250
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                                                                                                                                                                                                                                                         hypothetical protein F45H11.1 - Caenorhabditis elegans (;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T22250
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A;Residues: 1-234 <FIS>
A;Cross-references: EMB
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C;Keywords: glycosidase; hydrolase
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A;Molecule type: DNA
A;Residues: 1-1049 <EAD>
A;Cross_references: EMBL:AF016850; NID:g2407175; PII
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                                                                                                     A; Experimental source: clone F45H11
                                                                                                                   A;Cross-references: EMBL:Z78420; PIDN:CAB01709.1; GSPDB:GN00019; CESP:F45H11.1
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nilarity 55.6%;
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A;BCEALUS. FILE DNA
A;Molecule type: DNA
A;Residues: 1-533 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB75881.1; PID:g17133317; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Wata Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yas DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2328
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Science 294, 2317-2333, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Respan, W.; Perry, M.; Perry, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2,3-bisphosphoglycerate-independent phosphoglycerate mutase [imported] - Nostoc (Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AG3328
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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A; residues: 1-361 <KUR>
A; residues: 1-361 <KUR>
A; Cross-references: GB:AE008687; PIDN:AAL46002.1; PID:g17743757; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
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;Gene: fepD
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A; Dialis. Fig. DNA
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A;Residues: 1-188 <STO>
A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB06854.1; GSPDB:GN00
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A33650; MUID:20512582; PMID:11058132
A;Accession: G84041
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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujil, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185
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A;Cross-references: GB:AL590842; PIDN:CAC92694.1; PID:g15981389; GSPDB:GN00175
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PhnP protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Dec-2002
C;Accession: AB0421
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                                                                                                                                                                                                  Title: Genome sequence of Yersinia pestis, the causative agent of plague, Reference number: AB0001; MUID:21470413; PMID:11586360, AB0421
                                                                               ;Status: preliminary
;Molecule type: DNA
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Search completed: January 29, Job time: 12.1176 secs

2004, 14:58:23

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A;Molecule type: DNA
A;Residues: 1-255 <GLA>
A;Residues: 1-255 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC98754.1; PID:g16410065; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
                                                                                                                                                                                                                                                                           Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1159
                                                                                                                                                                                                                                                                                                                                                                                                flagellar biosynthesic protein FliP homolog lmo0676 (imported) - Listeria monocytogen
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AD1159
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
; Dominguez-Bernal, L.; Buchrieser, C.; Amend, A.; Dussurget, O.; Entian, K.D.; Fsihi,
D.; Jones T. M.; Karet T.
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                                                                                                                                     A; Gene: 1mo0676
C; Superfamily:
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C;Superfamily: ATP-binding protein PhnP
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Listing first 45 summaries
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39
1 GVNAXSALF 9
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Copyright (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

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his SWISS-PROT entry is copyright. It is produced through a colletween the Swiss Institute of Bioinformatics and the EMBL ou he European Bioinformatics Institute. There are no restriction see by non-profit institutions as long as its content is its incitied and this statement is not removed. Usage by and for notities requires a license agreement (See http://www.isb-sib.ch		-:- FUNCTION: PRESENTS CARBOHYDRATE LIGANDS TO SELECTINS. ALSO IMPLICATED IN TUMOR CELL METASTASIS!- SUBCELLULAR LOCATION: Type I membrane protein. LysosomalTHIS PROTEIN SHUTTLES BETWEEN LYSOSOMES, ENDOSOMES, AND THE PLASMA MEMBRANE.	≀-associated memb	SEQUENCE OF 25-406 FROM N.A.; AND PARTIAL SEQUENCE. MEDLINE=88243732; PubMed=3379044; Chen J.W., Cha Y., Yuksel K.U., Gracy R.W., August J.T.; Chen n., Cha Y., Yuksel K.U., Gracy R.W., August J.T.; "Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycoprotein mouse LAMP-1. Sequence similarity to proteins bearing onco-differentiation antigens."; J. Biol. Chem. 263:8754-8758(1988).	121 SEQUENCE FROM N.A. Heffernan M., Yousefi S., Dennis J.W.; Submitted (FEB-1990) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A. MEDLINE=90307738; PubMed=2142158; MEDLINE=90307738; PubMed=2142158; MEDLINE=90307738; PubMed=2142158; Mellanius A.; Melenius A.;	LAMPI OR LAMP-1. Mus musculus (Mouse). Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. MCBI TaxID=10090; [1]	; 🗗

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RESULT 2
LMP1_RAT
ID LWP1
AC P1456
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DT 01-WA
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DE KDA 1
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EMBL; M25244; AAA39869.1; -.
EMBL; J03881; AAA39411.1; -.
PIR; AA8067; A28067.
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MGD; MGJ:96745; Lamp1.
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Pfam; PF01299; Lamp; 1.

PRINTS; PR00336; LIVANSSOCTDMP.

PROSITE; PS00310; LAMP 1; 2.

PROSITE; PS00311; LAMP 2; 1.

Transmembrane; Glycop,
                                                           TMP1 RAT STANDARD; PRT; 407 AA.

P14562; P97620;

01-JAN-1990 (Rel. 13, Created)

01-JON-1990 (Rel. 13, Last sequence update)

01-NOV-1997 (Rel. 35, Last annotation update)

Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1)

kDa lysosomal membrane glycoprotein) (LGP-120) (CD107A).

LAMP1 OR LAMP-1.
               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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N-LINKED GLCNAC...) 
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Pred. No. 6.5;
2; Mismatches
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6.5;
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Transmembrane; SIGNAL 1
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SEQUENCE FROM N.A.
MEDLINE=89017240; PubMed=3174652;
Granger B.L., Hull M.,
                                                                      CARBOHYD
CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams L.A., Werny I., Schwartz S.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PRESENTS CARBOHYDRATE LIGANDS TO SELECTINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation and sequencing of a sialoglycoprotein in rat liver FEBS Lett. 244:351-356(1989).
                                                                                                                                                                                                                                                                                                                                            EMBL; M34959; AAA41525.1; -. EMBL; X14765; CAA32873.1; -. EMBL; U75406; AAB19108.1; -. PIR; A30200; A30200.
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                                                            CARBOHYD
                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                    PROSITE; PS00310; LAMP_1; PROSITE; PS00311; LAMP_2;
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Sakaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE OF 283-357 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMPLICATED IN TUMOR CELL METASTASIS.
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  Glycoprotein;
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  LUMENAL (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL)

FIRST LUMENAL DOMAIN.

HINGE.

SECOND LUMENAL DOMAIN.

BY SIMILARITY.

BY SIMILARITY.

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BY SIMILARITY.

N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)
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28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Probable manganese transport protein mntH.
MNTH OR ALL7601.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
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Plasmid pCC7120beta.
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
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TIGRFAMs; TIGR01197; nramp; 1.
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                                                                          Fransport;
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SUBCELLULAR LOCATION: Integ
(Probable).
SIMILARITY: BELONGS TO THE
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Pfam; PF01676; Metalloenzyme; I.

"No, PD004429; Pgm bpd ind; I.

"No, TIGR01307; Pgm bpd ind; I.

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Q8YPL2;
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura 1
Kishida Y., Kohara M., Matsumoto M., Matsuno A.,
Makazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).

1- FUNCTION: Catalyzes the interconversion of 2-phosphoglyce
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
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RESULT 5
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01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: BINDS TO THE F' ELEM
REPRESS ITS TRANSCRIPTION.
-i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: BELONGS TO THE TALL
-i- SIMILARITY: Contains 1 homeobo
                                                                                                                                                               ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1;
                                                                                                                                                                                                 PIR; S58439; S58439.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
MEDLINE=95396587; PubMed=7667102;
Ryan A.K., Tejada M.L., May D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last samotation update)
128-FBB-2003 (Rel. 41, Last annotation update)
Homeodomain protein AKR (Avian knotted-related
Gallus gallus (Chicken)
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                                                                                                                                                   PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG PROSITE; PS50071; HOMEOBOX_2; 1.
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                                                                                                                          Nuclear protein.
                                                                                                                                    Transcription regulation; Repressor; Homeobox; DNA-binding;
                                                                                                                                                                                                                                         EMBL; U25353; AAA83567.1;
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66.7%;
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Pred. No.
                                                             Score 29;
Pred. No.
                                                                                                  HOMEOBOX (TALE-TYPE); 1074355DCC0C2253 (
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n homeodomain
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RESULT 6
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RA STOULO
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RA GALLI
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RX MEDLINE-21848401; PubMed=11859360;
RA MOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Golins M., Eart N., Hayles J., Basham D., Bowman S.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Goliver K., Jones M., Fearson D., Quail M.A., Rabbinowitsch E.,
RA Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Ritherford K., Ritter S., Saunders D., Seeger K., Sharp S.,
RA Ritherford K., Ritter S., Saunders D., Seeger K., Sharp S.,
RA Ritherford K., Ritter S., Saunders D., Seeger K., Sharp S.,
RA Ritherford K., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Beer P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Gerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RI Nature 415:817.880 (2002).
C. --- SUMCELULAR Location: Type II membrane protein. Golgi (Potential).
C. --- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 34.
      Query Match
Best Local S
Matches
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01-NOV-1995 (Rel. 32, Last sequ
28-FEB-2003 (Rel. 41, Last anno
Putative glycosyl transferase Cl
SPAC5H10.13C.
                                                                                                                 DOMAIN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z49811; CAA89963.1; ~. PIR; T38977; S55491.
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r; Golgi stack; Glycoprotein.
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/lycoprotein.
/CYTOPLASMIC (POTENTIAL)
                                                                                                                                                      N-LINKED
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                                                                                                                                                                                                                                     (POTENTIAL).
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(GLCNAC...
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RESULT REPORT OF THE PROPERTY 
RESULT 8

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AC QBDC74;

DT 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DT 15-SEP-2003 (Rel. 42, Created)

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HAMAP; MF 00003; -; 1.
Pfam; PF02033; RBFA; 1.
ProDom; PD007327; RLb bind fact
TIGRFAMS; TIGR00082; FbfA; 1.
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MEDLINE=22598143; PubMed=12712204;

Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,

Ren S.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,

Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-H., Yin H.-F.,

Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,

Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,

Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,

Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,

Xu J.-G., Zhao G.-P.;
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15-SEP-2003
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Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGR00082; rbfA; PROSITE; PS01319; RBFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8F7K0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Event European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content infinite and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Associates with free 30S ribosomal subunits (but not with 30S subunits that are part of 70S ribosomes or polysomes). Essential for efficient processing of 16S rRNA. May interact with the 5'terminal helix region of 16S rRNA (By similarity). SUBCELLULAR LOCATION: Cycoplasmic (Potential). SIMILARITY: BELONGS TO THE RBFA FAMILY.
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5; Conserv
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55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB:
Pred. No. 15;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 117;
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strictions on its
t is in no way
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                                                        W. MEDLINE-20504483; PubMed=11016950;

W. MS W. V., Kennedy S. P., Mahairas G.G., Berquist B., Pan M.,

A Shukla H. D., Lasky S. R., Baliga N. S., Thorsson V., Sbrogna J.,

A Swartzell S., Weir D., Hall J., Dahl T. A., Welti R., Goo Y. A.,

A Leithauser B., Keller K., Cruz R., Danson M. J., Hough D. W.,

A Leithauser B., Keller K., Cruz R., Danson M. J., Hough D. W.,

A Leithauser B., Feller K., Frebs M. P., Angevine C. M., Dale H.,

A Lam M., Freitas T., Hou S., Daniels C. J., Dennis P. P., Jung K.-H

A Alam M., Freitas T., Hou S., Daniels C. J., Dennis P. P., Omer A.D.,

A Alam M., Lowe T. M., Liang P., Riley M., Hood L., DasSarma S.;

T'Genome sequence of Halobacterium species NRC-1.";

T'Genome sequence of Halobacterium species NRC-1.";

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

-!- FUNCTION: Catalyzes the NADPH-dependent reduction of ketopantoate into pantoic acid (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 5
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HAWAP; MF 00201; -; 1.
InterPro; IPR003717; RecO.
Pfam; PF02565; RecO; 1.
DNA repair; DNA recombination; C
SEQUENCE 243 AA; 27570 MW; 6
                                                                                                                                                                                                                                                                                                                                             Halobacterium sp. (strain NRC-1 / ATCC
Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative 2-dehydropantcate 2-reductase (EC 1.
reductase) (KPA reductase) (KPR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HALN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome seque Submitted (DEC-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
NCBI TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhee J.H.,
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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(By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE RECO FAMILY.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PANE HALNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
PATHMAY: Pantothenate blocynthesis.
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: BELONGS TO THE KETOPANTOATE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 GINLYSALY
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence of Vibrio vulnificus CMCP6.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA repair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB Pred. No. 33; 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                ATCC 700922 / JCM 11
ria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and recF
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                                                               2-dehydropantoate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jeong
   FAMILY
                                                                                              of ketopantoate
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REPRESENTATION OF THE PROPERTY OF THE PROP
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GCP_BAC
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        W. MEDLINE-98044033; PubMed=9384377;

XX. Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

XX. Kunst F., Ogasawara N., Moszer I., Albertini A., Borchert S.,

XX. Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

XX. Borriss R., Bourster L., Brans A., Braun M., Brignell S.C., Bron S.,

XX. Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

XX. Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

XX. Tritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

XX. Glims X.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

XX. Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

XX. Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

XX. Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

XX. Aurita K., Koetter P., Koningstein G., Krogh S., Kumano M.,

XX. Kurita K., Lapidus A., Lardnois S., Lauber J., Lazarevic V.,

XX. Medina N., Mellado R.P., Miznno M., Mosetl D., Makai S., Noback M.,

XX. Medina N., Mellado R.P., Miznno M., Mosetl D., Makai S., Noback M.,

XX. Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches
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005518;
15-JUL-1998
15-JUL-1998
28-FEB-2003
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ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence and analysis of the Bacillus subtilis chromosome."; Microbiology 143:1861-1866(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=168 / JH642;
MEDLINE=97346038; PubMed=9202461;
Sadaie Y., Yata K., Fujita M., Sagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003710; ApbA.
Pfam; PF02558; ApbA; 1.
TIGRFAMS; TIGR00745; apbA_panE; 1.
Hypothetical protein; Pantothenate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probable O-sialoglycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ogasawara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
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D84230; D84230.
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GINAATAL 198
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endopeptidase (E
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Pred. No. 42;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EC
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RESULT 11

KSS5_ECOLI

ID KSS5 ECOLI

AC P42218;
DT 01-NOV-1995 (
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Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Raynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium Bacillus"
STRAIN=K5;
STRAIN=93388530; PubMed=8397187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Subtilist; BG12202; gcp.
InterPro; IRR000905; Peptidase M22.
Pfam; PF00814; Peptidase M22; I.
PRINTS; PR00789; OSIALOPTASE.
PRODOM; PD002367; Peptidase_M22; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D88802; BAA19718.1; -.
EMBL; Z99107; CAB12413.1; -.
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                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                Enterobacteriaceae;
NCBI_TaxID=562;
                                                                                                                                                                                                  Bacteria; Proteobacteria;
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MEROPS; M22.UPW; --.
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CATALYTIC ACTIVITY: Hydrolysis of O-sialoglycoproteins;
31-Arg-|-Asp-32 bond in glycophorin A. Does not cleave
unglycosylated proteins, desialylated glycoproteins or
glycoproteins that are only N-glycosylated.
COTACTOR: ZINC (PROBABLE).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M22.
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-1995 (Rel. 32, L:
-1995 (Rel. 32, L:
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, Last sequence upo
, Last annotation of
de export protein )
                                                                                                                                                                                                     Gammaproteobacteria;
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Pred. No. 4
0; Mismatc
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(See http://www.isb-sib.ch/announce/
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Cell. Mol
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_CRIGR
EMBL; L18986; AAC37682.1; -.
InterPro; IPR002000; Lamp.
Pfam; PF01299; Lamp; 1.
PRINTS; PR00336; LYSASSOCTDMP
PROSITE; PS00310; LAMP_1; 2.
                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL. the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.orsend an email to license@isb-sib.ch).
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PIR; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=97021428; PubMed=8867788;
Uthayakumar S., Granger B.L.;
"Cell surface accumulation of overexpressed hamster membrane glycoproteins.";
Cell Mol Biol Bes 41.405.420(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10029;
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Eukaryota; Metazoa; Chordata; Crania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular analysis of region 1 of the Escherichia gene cluster: a region encoding proteins involved expression of capsular polysaccharide.";
J. Bacteriol. 175:5978-5983 (1993).
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"Molecular analysis
gene cluster: a regi
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SEQUENCE 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. MOI. Biol. Res. 41:405-420(1995).
FUNCTION: PRESENTS CARBOHYDRATE LIGANDS TO SELECTINS.
IMPLICATED IN TUMOR CELL METALS: (BY SIMILARITY).
SUBCELLULAR LOCATION: Type I membrane protein. Lysoson
THIS PROTEIN SHUTTLES BETWEEN LYSOSOMES, ENDOSOMES, AN
MEMBRANE (BY SIMILARITY).
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transport; Transport.
AA; 46381 MW; 73058122C28027DE
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Pred. No.
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P44565;
01-NOV-1995
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STRAINARd / KW20 / ATCC 51907;

MEDLINE=95350630, PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness I Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick Carlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Gocayne J.D., McKenney K., Sutton G., Fitzhugh M., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D. Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R. Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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DOMAIN
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Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                       0-succinylbenzoic
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5 (Rel. 32, Last sequence upd.
)3 (Rel. 41, Last annotation u
lbenzoic acid--CoA ligase (EC
"henzoate-CoA synthase).
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Pred. No. 58;
2; Mismatches
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BY SIMILARITY.
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(POTENTIAL)
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01-MAR-1989
01-MAR-1989
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                         LT 14
_HSV11
_VPAP_1
  MEDLINE=91056567; PubMed=2173776;
Gottlieb J., Marcy A.I., Coen D.M
"The herpes simplex virus type 1"
                                                             MEDLINE=88091053; PubMed=2826807; McGeoch D.J., Dalrymple M.A., Dolan Taylor P., Challberg M.D.; "Structures of herpes simplex virus replication of virus DNA."; J. Virol. 62:444-453(1988).
                                                                                                                                                             McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame McNab D., Perry L.J., Scott J.E., Taylor P., "The complete DNA sequence of the long unique region in the herpes simplex virus type 1.", "Gen. Virol. 69:1531-1574(1988).
                                                                                                                                                                                                                                                           Herpes simplex virus (type 1 / st
Viruses; dsDMA viruses, no RNA st
Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=10299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00501; AMP-binding; 1.

Pfam; PF0051TE; PS00455; AMP_BINDING; 1.

Menaquinone biosynthesis; Ligase; Complete proteome.

Menaquinone biosynthesis; AMP_BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
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"Whole-genome random sequencing and a Rd.";

Science 269:496-512(1995).

-!- FUNCTION: O-SUCCINYLBENZOIC ACID (OSB-COA).
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=88274327; PubMed=2839594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; HI0194;
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                                      FUNCTION.
                                                                                                                                       SEQUENCE FROM N.A.
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PATHWAY: Menaquinone biosynthesis.
SIMILARITY: BELONGS TO THE ATP-DEPENDENT
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R-1989 (Rel. 10, Last sequence update)
-2003 (Rel. 42, Last annotation updat
lymerase processivity factor (Polymer
(DNA-binding protein UL42).
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Coen D.M., Challberg M.D.;
type 1 UL42 gene product:
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EMBL; M1912; AAA45824.1; -.
PIR; D2980; WMB42.
PDB; 1DML; 15-WAR-00.
InterPro; IPR003202; UL42.
Pfam; PF02282; UL42.
Pfam; PF02282; UL42; 2.
DNA-binding; DNA replication; 3)
SEQUENCE 488 AA; 51159 MW;
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P12676;
01-0CT-1989
01-0CT-1989
15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase that functions to increase processivity.";
J. Virol. 64:5976-5987(1990).
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                                                                                                                                                                                                 Yue Q.K., Kass I.J., Sampson N.S., Vrielink A., "Crystal structure determination of cholesterol Streptomyces and structural characterization of mutants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHOA
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                                                                                                                                                                       Biochemistry 38:4277-4286(1999)
-!- CATALYTIC ACTIVITY: Cholesterol
                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS), MEDLINE=99211873; PubMed=10194345;
                                                                                                                                                                                                                                                                                                    Streptomyces sp.";
J. Bacteriol. 171:596-601(1989)
                                                                                                                                                                                                                                                                                                                            MEDIINE=89123081; PubMed=2914858;
Ishizaki T., Hirayama N., Shinkawa
"Nucleotide sequence of the gene fo
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=89123081;
                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces sp. (strain SA-COO).

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cholesterol
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FUNCTION: ACCESSORY SUBUNIT OF THE DNA POLYMERASE THAT ACTS TO INCREASE THE PROCESSIVITY OF POLYMERIZATION
SIMILARITY: TO OTHER HERPESVIRUSES POLYMERASE ACCESSORY PROTEIN.
                                                                                     SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.
                                                                                                                        COFACTOR: FAD.
PATHWAY: CHOLESTEROL METABOLISM
                                                                                                                  SUBUNIT:
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(Rel. 12, Last sequence update)
(Rel. 42, Last annotation updat
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                                                                                                                  Monomer
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                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (strain SA-COO)
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432974563DF0A81B CRC64;
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TIGREAMS; TIGRO1409; TAT_signal seq; 1.
PROSITE; PS00623; GMC_OXRED_1; I.
PROSITE; PS00624; GMC_OXRED_2; FALSE_NEG.
Oxidoreductase; Signal; Flavoprotein; FAD; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDB; IIJH; 28-DEC-01.
PDB; IMXT; 25-FEB-03.
INCERPYC; IPR000172; GMC_oxred.
INCERPYC; IPR006311; Tat.
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PDB; 1B4V; 06-JAN-99
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or send an email to license@isb-sib.ch).
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E->Q: REDUCED ACTIVITY.
H->N,Q: REDUCED ACTIVITY.
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FAD (ADP PART) (POTENTIAL).
PROTON ACCEPTOR.
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Job time : 6.82353 secs
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Listing first 45 summaries
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate

6: sp_mammal:*

7: sp_mtc:*

8: sp_organelle:*

9: sp_phage:*
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Gapop 10.0 , Gapext 0.5
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                                                            sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	60	7	6	ហ	4.	LJ.	N	₽	Result No.
30	30	30	30	31	31	31	31	31	31	32	32	32	32	32	33	Score
					79.5							82.1	\sim	82.1	84.6	Query Match 1
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ALIGNMENTS

RESULT 1

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רטווט אפרם "טדררפטוופי.	AP003135; BAB43124.1;	AP003364: BAR58199	EMBT: AF001780: AAB63065.1: -		le sequencing of meticillin	Ogasawara N., Hayashi H., Hiramat	Yamashita A., Oshima K., Furuya K., Yoshir	K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,	·Ui Y., Takahashi N.K., Sawano T., Inoue RI., Kaito	i M., Matsumaru H., Maruyama A., Murakami H., Hos	1., Aoki KI., Nagai Y., Lian JQ., Ito T.,	., Uchiyama I., Baba T., Yuzawa	; PubMed=11418146;	SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);	SEQUENCE FROM N.A.		997).	acterial interference c	Novick R.F.;	MEDLINE=97342847; PubMed=9197262;		SEQUENCE FROM N.A.		3879, 1280;	icutes;	aure	aureus (strain N315), and	aureus (strain M	AGRD OR SAV2037 OR SA1842.1 OR SAS066.	protein).	(TrEMBLrel. 20, Last annotation	38t	(TrEMBLrel.	3586;	800

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RESULT 3
Q922T9
ID Q922
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                                                                                                                                                                                                                                  Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006785; AAH06785.1; -.
InterPro; IPR002000; Lamp.
Pfam; PF01299; Lamp; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to lysosomal membrane glycoprotein 1 (Fragment).
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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la T., Hashimoto N.,
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Submitted (DEC-2001) to the EMBI
EMBL; AY069968; AAL58070.1; -.
InterPro; IPR002000; Lamp.
Pfam; PF01299; Lamp; 1.
PR.NTS; PR00336; LYSASSOCTDMP.
PROSITE; PS00310; LAMP_1; 2.
PROSITE; PS00311; LAMP_2; 1.
SEQUENCE 406 AA; 43879 MW; C
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Q9DC13;
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Mammalia; Eutheria;
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STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851;
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Mammalia; Eutheria;
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01-MAR-2003 (TrEMBLrel. 23, Created)
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01-MAR-2003 (TrEMBLrel. 23, Last anno
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Clycerol-3-phosphate dehydrogenase.
TLL2111.
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InterPro; IPR002000; Lamp.
Pfam; PF0129; Lamp; 1.
PRINTS; PR00336; LYSASSOCTDMP.
PRINTS; PS00310; LAMP_1; 2.
PROSITE; PS00311; LAMP_2; 1.
SEQUENCE 407 AA; 43936 MW;
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01-JUN-2002
01-JUN-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 25586;

MEDLINE=21886394; PubMed=11889109;

Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidi Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Basieva O., Chu L., Xogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.;

"Genome sequence and analysis of the oral bacterium Fusobacteri nuclearum strain ATCC 25586.";
                                                                                                                                                                                                                                              Synechococcus elongatus Bacteria; Cyanobacteria;
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eptidase (EC 3.4.13.3).
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RX KEDILINE-98044033; PubMed=9384377;

RA KEDILINE-98044033; PubMed=9384377;

RA Azevedo V. Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Deriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Britz C., Fujita M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Ghiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Gilseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Gilseppi G., Guy B.J., Haga K., Haiech J., Krogh S., Kumano M.,

RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Moone D., Oveilly M., Ogawa K., Ogiwara A., Oudega B., Paak S. H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Parro V., Pohl T.M., Schleich S., Schroeter R., Scoffone F.,

RA Setiguchi J., Seconia E., Rache B., Rose M., Sadaie Y.,

RA Setiguchi J., Seconia E., Takagi T., Takahashi H., Takamaru K.,

RA Viania A., Wambutt R., Wedler E., Wannier F., Vassarotti A.,

RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasamoto K., Yata K.,

Yata A., Yashikawa H., J. Zumstein E., Yoshikawa H., Danchin A.,

RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasamoto K., Yata K.,

RA Winters P., Wata A., Farler of the Gram-rositive batterium Bacillus
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01-JAN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Bacteria; Firmicutes;
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Nature 390:249-256(1997)
[2]
                                                               "The complete genome sequence subtilis.";
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Gene 194:91-196(1997)

EMBL; Z99108; CAB12580.1; -.

EMBL; Z99108; CAB12581.1; -.

Interpro, IPR000522; FecCD.

Pfam; PF01032; FecCD; 1.
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STRAIN=168;
Kunst F., Ogasawara
Submitted (NOV-1997
[3]
SEQUENCE FROM N.A.
STRAIN=AC327;
                                                                                                             Q9PKY0
Q9PKY0;
01-OCT-2000
01-OCT-2000
01-JUN-2002
Chlamydia muridarum.
Bacteria; Chlamydiae;
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2002) to the EMBL; AE011238; AAN47723.1; Complete proteome. SEQUENCE 493 AA; 54728 MW
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Bacteria; Spirochaetes;
NCBI TaxID=173;
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                                                                                                             ) (TrEMBLrel. 1
) (TrEMBLrel. 1
) (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             79.5%;
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66.7%;
                                 Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                           15, Created)
15, Last sequence update)
21, Last annotation updat
FHIPEP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spirochaetales;
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Last anno
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Pred. No.
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Pred. No. 82;
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the 70 degree-73 degree region
genes for a new two-component
genes for a new two-component
                                                                                                                                                                                                                                                                                                                                                                                                               DB 16;
1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 493;
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N [1]

P. SEQUENCE FROM N.A.

P. STRAIN=MOPn / Nigg;

C. STRAIN=MOPn / Nigg;

RX MEDIINE=20150255; PubMed=10684935;

RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.

RA White O., Hickey E.K., Peterson J., Utterback T., Berry K.,

Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dods

RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Sal

RA Eisen J., Fraser C.M.,

"Genome sequences of Chlamydia trachomatis MoPn and Chlamyd

"nneumoniae AR39.";

"nneumoniae AR39.";
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Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 6
                                                                                                                                                                                             InterPro; IPR001092; HLH_basic.
InterPro; IPR001610; PAC.
InterPro; IPR0001611; PAS_domain.
InterPro; IPR000014; PAS_domain.
Pfam; PF00010; HLH; 1.
Pfam; PF00785; PAC; 1.
Pfam; PF00999; PAS; 1.
SMART; SM0036; PAC; 1.
SMART; SM0036; PAC; 1.
SMART; SM00091; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                 structure in the aryl hydrocarbon rece
tetrachlorodibenzo-p-dioxin-resistant
Mol. Pharmacol. 54:86-93 (1998).
-i- SIMILARITY: BELONGS TO THE BASIC PERANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE002301; AAF73547:1; -.
TIGR; TC0330; -.
Intern-
                                                                                                                              PROSITE; PS00038;
PROSITE; PS50888;
PROSITE; PS50112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Han/Wistar;
MEDLINE=98325247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              088930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001712; Bact_FHIPEP Pfam; PF00771; FHIPEP; 1.
PRINTS; PR00949; TYPE3IMAPROT.
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF082124; AAC35168.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okey A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aryl hydrocarbon receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Point mutation in intron sequence causes altered carboxyl-terminal structure in the aryl hydrocarbon receptor of the most 2,3,7,8-tetrachlorodibenzo-p-dioxin-resistant rat strain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pohjanvirta R., Wong
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Similarity 55.05; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 6; Conser
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                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; (Rat).
pa; Chordata;
ia; Rodentia;
                                                                                                                              HLH_1;
HLH_2;
PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9658193;
ong J.M.Y., Li W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   φ
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                       79.5%;
55.6%;
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Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
  Score 31; DB 11
Pred. No. 2e+02;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                           BASIC HELIX-LOOP-HELIX
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                                            DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                          Length 810;
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                                                                                        CRC64;
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    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                             (BHLH) FAMILY
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Dodson R.,
Salzberg S.L.,
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Query Match
Best Local S
Matches 5
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01-JAN-1998
01-MAR-2003
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013344;
                                                                                                                        NON TER
                                                                                                                                            Pfam; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eades C.J., Gilbert A., Goodman C.D., Hintz W.E.;

"Identification and analysis of a class 2 alpha-mannoside
Aspergillus nidulans.";

Glycobiology 0:0-0(1997).

EMBL; AF016850; AAB70514.1; -.

EnterPro; IPR000602; Glyco.hydro_38.

InterPro; IPR000601; SBP_Odom1.

Pfam; PF01074; Glyco.hydro_38; 1.

PROSITE; PS01037; SBP_BACTERIAL 1; 1.

SEQUENCE 1049 AA; 118684 MW; 7306F27ECA8A999B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Perizomycotina;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q50375
Q50375;
Q1-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                 "Identification of genes involved in the sequestration of imycobacteria: The ferric exochelin biosynthetic and uptake Mol. Microbiol. 14:557-569(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium smegmatis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha-mannosidase.
MSD2.
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=mc6;
MEDLINE=95191405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=T
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                                                                                                                                                                                                                        nterPro;
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                                                                                                                                                                                                                     Microbiol. 14:557-569(1994).
, U10425; AAC43258.1; -.
xPro; IPR000522; FecCD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    979
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                                                                                                                                                                                       PF01032; FecCD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-1
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Similarity
5; Conserve
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7; Conserva
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GINSQSAMF
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      Conservative
                                                                                                                           AA;
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                          76.9%;
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; Score 30; DB 2; Pred. No. 97; 3; Mismatches
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class 2 alpha-mannosidase
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C STRAIN=13 / Type A;

X PubMed=11792842;

X PubMed=11792842;

X PubMed=11792841;

A Shima T., Ottani K., Hirakawa H., Ohshima K., Yamashita A.,

A Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;

A Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;

T (Complete genome sequence of Clostridium perfringens, an anae

T (Templete genome sequence of Clostridium perfringens, an anae

T (Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

IR EMBL; AP003188; BAB80518.1; -.

IR EMBL; AP003188; BAB80518.1; -.

IR InterPro; IPR001993; Mitoch_carrier.
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Best Local S
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Science 282:2012-2018(1998).
Science 282:2012-2018(1998).

EMBL, Z78420; CAB01709.1; -.

Wormbeg; F45H11.1; CE1655.

InterPro; IPR007087; Znf_C2H2.

Pfam; PF00096; zf-C2H2; I.

SMART; SW00355; Znf_C2H2; I.

PROSITE; PS00028; Znf_CFINGER_C2H2_1; 1.

PROSITE; PS000728; ZNC_FINGER_C2H2_2; 1.

Metal-binding; Zinc; Zinc-finger.

SEQUENCE 298 AA; 31721 MW; F83ESFE55
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Q93727;
Q1-FEB-1997
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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01-MAR-2003
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Clostridium perfringens.
Bacteria; Firmicutes; Clostridia;
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NCBI_TaxID=1502;
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Pred. No. 1.2e
1; Mismatches
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DR Pfam; PF01032; FecCD; 1.

DR ProDom; PD001557; FecCD; 1.

DR PROSITE; PS00215; MITOCH_CARRIER; 1.

KW Complete proteome.

SQ SEQUENCE 337 AA; 36437 MW; 565F8193B7BCB913 CRC64;

Query Match
Best Local Similarity 55.6%; Pred. No. 1.4e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSALF 9
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Db 96 GINSGAALF 104

Search completed: January 29, 2004, 14:56:50

Job time: 27.8676 secs
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Sequence 32, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 29, Appli Sequence 32, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 31, Appli Sequence 32, Appli Sequence 4, Appli

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Result
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length: 2000000000
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Match
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1: /ogn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /ogn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /ogn2_6/ptodata/1/iaa/6B_COMB.pep:*

4: /ogn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /ogn2_6/ptodata/1/iaa/6TUS_COMB.pep:*

6: /ogn2_6/ptodata/1/iaa/backfīles1.pep:*
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        GenCore version 5.1.6 (c) 1993 - 2004 Compugen
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US-09-189-930-141

US-09-189-930-141

US-09-189-930-241

US-09-189-930-241

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US-09-189-930-2572

US-09-189-189-2922

US-09-189-189-30-341

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US-09-189-18-2922-2

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  Sequence 6, Appli
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Sequence 141, Appli
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Sequence 27723, Appli
Sequence 2922, Appli
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Sequence 34, Appli
Sequence 3765, Ap
Sequence 38, Appli
Sequence 88, Appli
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APPLICANT: Mayville, Patricia
APPLICANT: Mo. 6337985ick, Richard P.
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
ITITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
ICURRENT APPLICATION UNMBER: 05/090,402
PRIOR FILING DATE: 1998-06-24

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US-09-339-511-1
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US-09-339-511-6
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Best Local S
Matches 9
      APPLICANT:
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                                                                                                  Sequence 1, Application Patent No. 6337385 GENERAL INFORMATION:
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Mayville, Patricia
No. 6337385ick, Richard E
Beavis, Ronald
Ji, Guangyong
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US-09-233-336A-6
US-09-233-752A-6
US-09-233-752A-6
US-09-402-036-6
US-09-471-033-29
US-08-471-044-32
US-08-471-044-32
US-08-471-046A-32
US-08-471-046A-32
US-08-470-566B-29
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Best Local S
Matches 7
                                                                        GENERAL INFORMATION:
APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN
FILE REFERENCE: 63753/7
CURRENT APPLICATION NUMBER: US/08/861,476C
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
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SEQ ID NO 1
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CURRENT APPLICATION NUMBER: US/08/861,476C
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
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CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 199-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0
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OTHER INFORMATION: Xaa represents any amino
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OTHER INFORMATION:
NAME/KEY: VARIANT
ORGANISM: Staphylococcus aureus
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77.8%;
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Best Local
SEQ ID NO 2
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Patent No.
                    FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
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CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
                                                                                                                                              APPLICANT:
                                                                                                     TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS
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ITLE OF INVENTION: NOVEL STAPHY
ITLE OF INVENTION: INTERFERENCE
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5. 6337385
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7; Conserv
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             PatentIn Ver. 2.0
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                                                                                                                                                             Mayville, Patri
No. 6337385ick,
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Mayville, Patri
No. 6337385ick,
                                                                                                                                    Ji, Guangyong
                                                                                                                                                 Beavis, Ronald
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85ick, Richard
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77.8%;
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Pred. No. 1.
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Pred. No.
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OTHER INFORMATION: Description of Artificial Sequence OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at US-09-339-511-7
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CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
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APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYI
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
                              APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
                                                                                      APPLICANT:
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NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'ILING DATE: 1
                                                                                                                                                                            4, Application US/09339511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Application US/09339511 6337385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 77.
                                                                                                                                                                                                                                                                                                                 Similarity 77. 7; Conservative
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                                                                                    No. 6337385ick,
Beavis, Ronald
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Mayville, Patricia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description of peptide
                                                                                                                    Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
                                                                                                                                                                                                                                                                                                                                74.4%;
77.8%;
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77.8%;
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                                                                                                      Richard P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                   Score 29; DB 4;
Pred. No. 2.5e+05;
1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Artificial Sequence: Synthetic
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 141 LENGTH: 322
                                                                                                                                                                              Sequence 141, Application US/09312283C Patent No. 6573095
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CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matchew
APPLICANT: Sleeman, Matchew
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER:
                   APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
RITLE OF INVENTION: Compositions Isolated from Skin Cells
RITLE OF INVENTION; and wethods for Their Use
                                                                                                APPLICANT:
                                                                                                                               APPLICANT: Watson, James
APPLICANT: Strachan, Lo
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                               305 GVNLFSCLF 313
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APPLICATION NUMBER: US/09/312,283C
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                                                                                                            Strachan, Lorna
Sleeman, Matthew
                                                                                                Onrust, Rene
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87.5%;
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66.7%;
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Pred. No. 2
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DAYE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
TYPE: PRT
COORMINE MATTER.
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APPLICANT: Palmer, Leslie M.
APPLICANT: Kosmatka, Anna L.
APPLICANT: Kosmatka, Anna L.
APPLICANT: Traini, Christopher M.
APPLICANT: Warren, Richard L.
TITLE OF INVENTION: 9cp
FILE REFERENCE: GM10166
CURRENT APPLICATION NUMBER: US/09/149,624
CURRENT FILING DATE: 1998-09-08
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 341
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US-09-188-930-341
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TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-149-624-2
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US-09-149-624-2
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; ORGANISM: Mouse
US-09-312-283C-141
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       Query Match
Best Local Similarity
Whiches 6; Conserve
                                                                                      ; ORGANISM: Mouse US-09-188-930-341
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity 66.7%;
Matches 6; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 141
LENGTH: 322
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Patent No. 61505
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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66.7%;
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Pred. No. 1.4e+02;
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                      Score 28; DB
Pred. No. 1.8e
0; Mismatches
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              DB 3;
1.8e+02;
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                                                       Length 431;
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5223391-9
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Best Local Similarity
Thes 6; Conserve
                    Sequence 25722, Application US/09252991A
Patent No. 6551795
PARENT INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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US-09-252-991A-25722
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CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 341
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Compositions Isolated from TITLE OF INVENTION: and Methods for Their Use FILE REFERENCE: 11000.1011c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 431
TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/482,634
FILING DATE: 21-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ent No. 5223391
APPLICANT: COEN, DONALD M.;DIGARD, PAUL E.
TITLE OF INVENTION: INHIBITIORS OF HERPES SIMPLEX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 488
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o. 6573095
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Sleeman, Matthew
Onrust, Rene
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66.7%;
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Pred. No. 1.8e+02;
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PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25722

LENGTH: 1380

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-25722

Query Match
Best Local Similarity 85.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps O;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps O;

Search completed: January 29, 2004, 15:03:22

Job time: 11.1176 secs
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Title:
Perfect score:
Sequence:
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length: 2000000000
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1 GVNAXSALF 9
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Gapop 10.0 , Gapext
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Maximum Match 100%
Listing first 45 summaries
Published_Applications_AA:*
/cgn2_6/ptodata/1/pubpaa
                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_RUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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8804 68808
8804 68808
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13
15
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          13 US-10-032-950-6
13 US-10-032-950-1
15 US-10-201-444-6
15 US-10-201-444-6
15 US-10-201-444-6
10 US-10-032-950-5
10 US-10-032-950-5
11 US-10-369-493-19084
12 US-09-882-227-184
12 US-09-882-227-184
13 US-10-032-950-7
15 US-10-104-502-12
15 US-10-104-502-12
15 US-10-132-574
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        Sequence 6, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 23, Appli
Sequence 19084, A
Sequence 184, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 12194, A
Sequence 12194, A
                                                                                                                      Sequence 6, 1
Sequence 3, 1
Sequence 6, 1
Sequence 5, 1
Sequence 3, 1
Sequence 3, 1
Sequence 3, 1
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ALIGNMENTS

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RESULT 1

US-10-032-950-6

; Sequence 6, Application US/10032950

publication No. US20020077433A1

; GENERAL INFORMATION:

APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Patricia
APPLICANT: Molecular Sequence
APPLICANT: Mayville, Patricia
APPLICANT: Molecular Sequence
FILE REFERENCE: 600-1-231N

CURRENT APPLICATION: NOVEL STARPH/LOCOCCUS PEPTIDES FOR BACTERIAL

TITLE OF INVENTION: NOVEL STARPH/LOCOCCUS PEPTIDES

FILE REFERENCE.

FILE REFERE
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                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 3 LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10201444
Publication No. US20030078378A1
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Best Local :
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                                                                             Matches
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Best Local :
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                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/201,444
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US/08/861,476
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: New York University Medical Center TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. FILE REFERENCE: 63753/7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position
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OTHER INFORMATION:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GVNAXSALF 9
                                      1 GVNAXSALF 9
                                                                         Similarity 7; Conserv
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                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description of Artificial Sequence: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                           84.6%;
77.8%;
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; Pred. No. 7e+0
1; Mismatches
                                                                                           Score 33; DB 15;
Pred. No. 7e+05;
                                                                             Mismatches
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RESULT 4 US-10-201-444-6

Sequence 2, Application US/10032950 Publication No. US20020077453A1 GENERAL INFORMATION: APPLICANT: Muir, Tom

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RESULT 6
US-10-032-950-2
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US-10-032-950-5
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; TYPE: PRT
; ORGANIEM: Staphylococcus aureus
US-10-201-444-6
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TITLE OF INVENTION: SLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE: 63753/7
CURRENT APPLICATION NUMBER: US/10/201,444
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US/08/861,476
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
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LENGTH: 9
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Publication No. US20030078378A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF 5EQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453Alick, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
                                                                                                                                                                                                                                                                                                                            LENGTH: 9
TYPE: PRT
ORGANIAM: Artificial Sequence
                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa represents any amino acid at this position
                                                                                                                                                                                                                                                    NAME/KEY: VARIANT LOCATION: (5)
                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: Description
OTHER INFORMATION: peptide
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                                                                                                                                         Similarity 77.8
7; Conservative
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                                                                                                                                                               79.5%;
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77.8%; Pred. No. 1.
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2; Mismatches
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RESULT 8
US-10-369-493-19084
; Sequence 19084, Application US/10369493
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CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-2
PRIOR APPLICATION NUMBER: PCT/NL99/00460
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: EP98202465.5
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
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SEQ ID NO 33
LENGTH: 388
TYPE: PRT
ORGANISM: Streptococcus suis
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CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 9
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satent No. US20020055168A1
serral information;
APPLICANT: Smith, Hilda
TITLE OF INVENTION; STREPTOCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPLICANT: J1, GUANGYONG
IITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Xaa represents any amino acid at this position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                      GVNGETALF 343
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No. US20020077453Alick, Richard P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .MBER: PCT/NL99/00460
1999-07-19
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77.8%;
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                                        RESULT 10
US-10-032-950-7
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Best Local S
Matches 5
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1984
LENGTH: 508
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 638
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 184
LENGTH: 549
Sequence 7, Application US/10032950 Publication No. US20020077453A1
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Publication No. US20030158396A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ocomen, Raymond P.

TITLE OF INVENTION: Identification of Polynuclectides
TITLE OF INVENTION: Encoding No. US20030158396Alel Helicobacter Polypeptides in
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/047002
CURRENT FALLIGATION NUMBER: US/09/882,227
CURRENT FILLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US/09/882,227
PRIOR APPLICATION NUMBER: US/08/902,615
PRIOR APPLICATION NUMBER: US 08/902,615
PRIOR FILING DATE: 1997-07-29
NUMBER OF TENER DATE: 1997-07-29
NUMBER OF TENER DATE: 1997-07-29
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
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Tomb, Jean-Francois
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larity 55.6%;
Conservative
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75.0%;
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Pred. No.
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Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                    Length 549;
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Mayville, Patricia No. US20020077453Alick, Richard

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FILE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 198-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: BB1470 US NA
CURRENT APPLICATION NUMBER: US/10/004,502
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,272
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 337
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Best Local Similarity
Thes 6; Conserve
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Best Local Similarity
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; COCHER INFORMATION: Xaa represents any amino acid at this position US-10-032-950-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/10004502 Publication No. US20030088882A1 GENERAL INFORMATION:
                                                                                                                    Sequence 9222, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Harvell, Leslie T. APPLICANT: Ragghianti, James J TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0-004-502-12
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                                                                                                      INFORMATION:
                                                                                                                                                                                                                            90 GVNAEGCLF 98
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              IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
 SAKAKI, YOSHIYUKI
                                                                                                                                                                                                                                                                                             Conservative
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66.7%;
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Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29; DB 13;
Pred. No. 7e+05;
1; Mismatches 1
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SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9222
LENGTH: 391
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Best Local Similarity
Watches 6; Conserve
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B JUNE FOR PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12194
LENGTH: 468
TYPE: PRT
                                                                                                                                    Sequence 574, Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
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APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL
FILE REFERENCE: 210121.469C8
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mesorhizobium loti
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Pred. No. 2e+02;
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                          FOR TREATMENT AND INFECTION
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APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453A1ick, Richard P.
APPLICANT: No. US20020077453A1ick, Richard P.
APPLICANT: No. US20020077453A1ick, Richard P.
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-7
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
OTHER INFORMATION: peptide
NAME/KEY: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-4
Search completed: January 29, 2004, 15:01:46 Job time: 25.5441 secs
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; LENGTH: 605
; TYPE: PRT
; ORGANISM: C. Trachomatis D serovar
US-09-841-132-574
                                                                                                                                                                                             Query Match 71.8%; Score 28; DB 13; Length 9; Best Local Similarity 87.5%; Pred. No. 7e+05; Matches 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10032950 Publication No. US20020077453A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.4%; Score 29; DB 9; Length 605; Best Local Similarity 66.7%; Pred. No. 2.7e+02; Matches 6; Conservative 1; Mismatches 2; Indels
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S. aureus peptide
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AgrD-autoinducing
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AgrD2 linear thioe
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ALIGNMENTS

Staphylococcus aureus infection; cyclic peptide; AgrD; agr response; virulence factor; treatment. S. aureus peptide #6 used for bacterial interference. Staphylococcus aureus. AAY67857 standard; peptide; (UYRQ) UNIV NEW YORK STATE (first entry) 98US-0103438 99WO-US14562 5 /label= Unknown /note= "N-terminal residue forms bond with C-terminal residue to form a cyclic peptide" Location/Qualifiers ø B

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RESULT 2
ABP53546
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Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a cyclic peptide derived from the Staphylococcus aureus AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
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Misc-difference
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                          New cyclic
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24-JUN-1999;
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                   infections
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) NOVICK R P.
) BEAVIS R.
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9; Conserv
Page
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99US-0339511
                                                                                                                                                                                                                                                                              Staphylococcus aureus;
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Matches
The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is a secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. Preferred peptides may have the sequence NH2-X(n)-Z-X(y)-COCH, with a cyclic bond between the Z residue and COOH other than a thioester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP53540 to ABP53547 represent cyclic peptides (I) from the present invention. The present invention also describes a method for treastably lococcus aureus infection comprising the administration of composition comprising (I). (I) has antibacterial activity, and coused as an agr gene response inhibitor. The peptides are useful fureating S. aureus infections.
                                                                                                                                                                                                           Claim 7;
                                                                                                                                                                                                                                                                                                                                            WPI; 2002-170774/22.
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                         peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
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example of the preparation of novel synthetic cyclic peptides of the invention (see AAM50899-906). The peptide corresponds to the staphylococcus aureus AgrDII sequence with a Cys5 to Ser mutation (lactone). It was synthesised on a Wang-resin using an Fmc (lactone). It was synthesised on a Wang-resin using an Fmc Walpha protection strategy. Following chain assembly, the peptide was cleaved from the support and the Ser-5 residue deprotected by treatment with a trifluoroacetic acid:anisole:water mixture (90:5:5) for 4 hr. The partially protected peptide-alpha (190:5:5) for 4 hr. The remaining protecting groups were then camposed by treatment with HF and the peptide by HPIC. The cyclic peptide is capable of inhibiting the agr response of Staphylococcus aureus. The thiololactone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring continuous continuous activity while preserving and continuous destroy agr response activating activity while preserving and confection inhibitory activity. The cyclic peptides are useful for infactorial interference, especially for the treatment of S. aureus
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Query Match Best Local

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                                                                               The present sequence is that of a novel synthetic AgrD2 linear chioester peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrB3 promoter. This allowed activation or inhibition of the agrB2 containing a beta-lactamase reporter gene fused to the agrB3 promoter. This allowed activation or inhibition of the agrB2 response to be monitored spectrophocometrically. Unlike an AgrB2 response to be monitored spectrophocometrically. Unlike an AgrB2 response to either activate or inhibit the agr response, even when added to cultured cells at uM concentrations. The invention provides claimed cyclic peptides (see AAM50899-906 and AAM50999) and methods for preparing them. The cyclic peptides are useful for information interference, especially for the treatment of S. aureus
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AAM51004 standard; Peptide; 9
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                                                                                                    Interior eyelic peptide in which residue 5 of the peptide is linked to residue 9 via a lactone bond. The peptide is derived from an AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agr3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. The lactone AgrD2 peptide inhibited the agr response of group I.s. aureus strains without activating the agr response in group I. II or III strains. The invention provides claimed cyclic peptides (see AMS0899-906 and AAMS0999) and methods for preparing them, especially peptides where the cyclic bond is a lactam or lactone bond. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus infection.
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                                                            Score 33; DB 23;
Pred. No. 9.3e+05;
                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beavis R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    residue 9 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              residue 5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J.
                                                                         Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               form
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RESULT 10

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RESULT 11
AAY67851
ID AAY
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AC AAY
AC AAY
AC AAY
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AC S. (
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DT 25-1
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
     Staphylococcus aureus infection; cyclic peptide; AgrD;
                                                    S. aureus peptide #1 used for bacterial interference.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulations are also provided. Methods using such AI-2 malogues are useful for a microorganism are also provided. Methods using such AI-2 malogues are useful for the provided of the provided of the microorganism are also provided. Methods using such AI-2 malogues are useful for the provided of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 33; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoinducer-2 receptor, regul
also antibiotic compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of autoinducer-2 agonists or antagonists autoinducer-2 receptor, regulating bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2000;
07-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200185664-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB07160
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                                                                                                      25-APR-2000
                                                                                                                                                     AAY67851;
                                                                                                                                                                                                     AAY67851 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-075235/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bassler BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (QUOR-)
(UYTE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quorum sensing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYPR-)
                                                                                                                                                                                                                                                                                                                                _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUOREX PHARM INC. UNIV TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                             GVNAXSSAF
                                                                                                                                                                                                                                                                                                                                GVNASSSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pheromone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-203000P.
2000US-254398P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-US15221
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                                                                                                   (first
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                                                                                                                                                                                                                                                                                                                                φ
                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.6%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibiotic; antibacterial; dermatological;
agr system; accessory gene regulator; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schauder'S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 23;
Pred. No. 9.3e+05;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for regulating activity growth and pathogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                             N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
     agr response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ptor, regulating compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                             0
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RESULT 12
AAY67861
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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus
                                                                        Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cyclic peptides for treating infections with Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09967286-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virulence factor; treatment
                    29-DEC-1999.
                                          WO9967286-A2
                                                                                                          Staphylococcus
                                                                                                                                 virulence
                                                                                                                                          Staphylococcus aureus infection; AgrD; agr response; treatment;
                                                                                                                                                              Staphylococcus aureus AgrDII derived peptide sequence
                                                                                                                                                                                      25-APR-2000
                                                                                                                                                                                                           AAY67861
                                                                                                                                                                                                                                 AAY67861 standard; peptide; 9
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 26; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-147202/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JW,
                                                                                                                                                                                                                                                                                                                                  Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                             GVNAXSSAF
                                                                                                                                                                                                                                                                                      GVNAXSSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mayville P,
                                                                                                                                                                                                                                                                                                                                                                              9 AA;
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aureus
                                                                                                          aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0103438
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                                                                /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Unknown
                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                                                           82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novick RP,
                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                             Score 32;
Pred. No.
                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            다.
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                                                                                                                                                                                                                                                                                                                                  9.3e+05;
ches 1;
                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beavis R;
                                                                                                                                                                                                                                                                                                                                                      Length 9;
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                   0
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24-JUN-1999;

99WO-US14562

-13

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ABP535XA

ABP535XX

ABP53

XX ABP53

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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-147202/13
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                                         Muir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP53540 standard; peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-1998;
WPI; 2002-681366/73
                                                                                                                        (MUIR/)
(MAYV/)
(NOVI/)
                                                                                                                                                                                                       24-JUN-1998;
24-JUN-1999;
                                                                                                                                                                                                                                                                     27-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                      US2002077453-A1
                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclic peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP53540;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    response
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                                         TW,
                                                                               ) MUIR T W.
) MAYVILLE P.
) NOVICK R P.
) BEAVIS R.
) JI G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    μ.
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8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVNAXSSLF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVNAXSSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mayville P,
                                         Mayville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROCKEFELLER
                                                                                                                                                                                                                                                                     2001US-0032950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; 37pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0103438
                                                                                                                                                                                                         98US-090402P.
99US-0339511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                             note=
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                                                                                                                                                                                                                                                                                                                                                                                           "any
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                                         Novick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB.
Pred. No. 9.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                             amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                         RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aureus; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ئ</u>.
                                         Beavis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
9.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cyclic peptides, useful for treating infections -
                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                  antibacterial;
                                                                                                                                                                                                                                                                                                                         Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                           AAM50899;
                                                                                                                                                                                                                                                                                                                                                                                           AAM50899 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating
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                                                                                                                                                                             08-JAN-2002.
                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                        AgrD-autoinducing cyclic peptide,
                                                interference
subject -
                                                         Novel synthetic, interference and
                                                                                                                                                            24-JUN-1999;
                                                                                                                                                                                             US6337385-B1
                                 Claim
                                                                                                                   (UYRQ ) UNIV
                                                                                                                                            24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as an agr gene response inhibitor. The peptides are useful for ting S. aureus infections.
                                                                                  2002-170774/22.
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8; Conserv
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                                 Column
                                                                                                  Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA;
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                                                                                                                   NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                  aureus; AgrD; agr response; infection; therapy; cyclic.
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                                                        cyclic AgrD-autoinducing peptide for bacterial for treating Staphylococcus aureus infection i
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88.9%;
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peptide"
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                                                                                                                                                                                                                                       peptide"
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Pred. No. 9.3e+05;
D; Mismatches 1
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The present sequence is that of a novel synthetic cyclic pe of the invention that is capable of inhibiting the agr resp Staphylococcus aureus. It is an AgrD-autoinducing peptide,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AgrD is a secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. Preferred peptides may have the sequence NH2-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z residue and COOH other than a thioester bond, where X is an amino acid, an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a synthetic or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-2002
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                                                                                                                                                                                                                                                                                                  Misc-difference
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                                          24-JUN-1999;
                                                                                         08-JAN-2002.
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24-JUN-1998;
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infection; therapy; cyclic.
98US-090402P
                                          99US-0339511
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/note=
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                                               Query Match
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Matches
                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 14; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection i
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GVNAXSSAF
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nilarity 88.9%;
Conservative
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Search completed: January 29, 2004, 14:52:13 Job time : 35.0735 secs

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Perfect score:
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protein search, using sw model
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length: 2000000000
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39
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1: pir1:*
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Listing first 45 summaries
 GVNAXSSAF 9
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Copyright (c) 1993 - 2004 Compugen Ltd
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C.Species: Staphylococcus aureus
C.Species: Staphylococcus aureus
C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C.Accession: C89995
R.;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89995
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C89995
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A;Molecule type: DNA
A;Residues: 1-47 <KUR>
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835071	G86349	H70662	A32225	S51574	G96713	S18597	C88571	F85056	S43574	AC0187	T04754	E86832	G86071	AF0915	A91225
auxin-resistance p	hypothetical prote	probable plcA prot	nerve growth facto	mock protein - Khi	-61	beta	C0585	tical prot	C05B5.3 protein (c	e iron-sid	Ę	oxidoreductase yrb	hypothetical prote	probable deoxyribo	E S

ALIGNMENTS

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RESULT 2
B95192
hypothetical protein SP1652 [imported] - Streptococcus pneumoniae (strain TIGR4)
c;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: B95192
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapplonson, T.; Hickey, S.K.; Holt, I.E.
science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris, A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris, A;Authors: Complete Genome Sequence of a virilent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-924 -KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75731.1; PID:g14973142; GSPDB:GN00164;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:BA000018; PID:g13701831; PIDN:BAB43124.1; GSPDB:GN00149
A;Experimental source: strain N315
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7; Conser
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Pred. No. 1.8;
0; Mismatches
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C: Date: 20'72-
C; Accession: A87066
R; Cole, S.T.; Eiglmeier, K.; Duthoy, S.; Felt:
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A; Authors: Rutter, S.; Seeger, K.; Simon, S.;
A; Title: Massive gene decay in the leprosy bac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C. A;Ticle: Genome of the Bacterium Streptococcus pneumoniae A;Accession: G98058
A;Accession: G98058
A;Status: preliminary
              RESULT 5
hypothetical
                                                                                                                                                       C;Genetics:
A;Gene: ML1255
A;Gene: ML1255
C;Superfamily: Mycobacterium leprae hypothetical protein MLCB1610.16
                                                                                                                                                                                                                                                      A;Reference number: A86909;
A;Accession: A87066
A;Status: preliminary
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A; Residues: 1-924 < KUR>
A; Cross-references: GB; C; Genetics:
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Matches 7
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Best Local S
Matches 6
                                                                                                                                                                                                                              ;Molecule type: DNA
;Residues: 1-163 <STO>
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Best Local
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protein
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6; Conser
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Rv2468c -
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77.8%;
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Mycobacterium
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Pred. No. 12;
0; Mismatches
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Pred. No. 45;
2; Mismatches
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Pred. No. 45;
2; Mismatches
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Feltwell, T.;
tuberculosis (strain H37RV)
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lysosomal membrane glycoprotein LAMP-1 - mouse C;Species: Mus musculius (house mouse) C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_cl C;Accession: A28067 R;Chen, J.W.; Cha, Y.; Yuksel, K.U.; Gracy, R.W.; August, J. Biol. Chem. 263, 8754-8758, 1988 A;Title: Isolation and sequencing of a cDNA clone encoding A;Reference number: A28067; MUID:88243732; PMID:3379044 A;Accession: A28067
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A;Molecule type: mRNA
A;Residues: 1-382 <CHE>
A;Cross-references: GB:J03881; NID:g198706; PIDN:AAA39411.1; PID:g293692
A;Note: the authors translated the codon ATT for residue 1 as Leu and CCC
C;Superfamily: lysosome-associated membrane protein
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein MLCB1610.16 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 28
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C;Superfamily:
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A;Residues: 1-167 <COL>
A;Cross-references: GB.AL021246; GB:AL123456; NID:g3261507; PIDN:CAA16045.1; PID:g279
A;Experimental source: strain H37Rv
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A;Accession: C70866
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C;Date: 17.7ul-1998 #sequence_revision 17.Jul-1998 #text_change 28-Jul-2000
C;Date: 10.7ul-1998 #sequence_revision 17.Jul-1998 #text_change 28-Jul-2000
C;Accession: C70866
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc
Connor, R.; Davies, R.; Deviln, K.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL049913;
A;Experimental source: cosmid B1610
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Best Local S
Matches 7
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Best Local
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77.8%;
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A;Molecule type: mRNA
A;Residues: 1-407 <HOWS
A;Residues: 1-407 <HOWS
A;Residues: 1-407 <HOWS
A;Cross-references: EMBLJ03672
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for residue 15 as Val
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A;Note: the authors translated the codon GGG 
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N;Alternate names: sialoglycoprotein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Oct-1989 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
C;Accession: A30200; S03331
C;Accession: A30200; Aaccession: A30200; Aaccession: A302000; Aaccession: A3020000; Aaccession: A302000000; Aaccession: A30200000000000000000000000000
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                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X14765; NID:g56577; PIDN:CAA32873 A;Note: part of this sequence, including the amino end of t C;Superfamily: 1ysosome-associated membrane protein C;Keywords: glycoprotein; membrane protein C;Keywords: glycoprotein; membrane glycoprotein, 107K #s1F;22-407/Product: lysosomal membrane glycoprotein, 107K #s1
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C; Superfamily:
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C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
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A;Residues: 22-407 <HIM>
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Best Local S
Matches 6
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: Derived protein sequence, oligosaccharides, and membrane insertion of
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A;Reference number: S02150; MUID:89104438; PMID:29:
A;Accession: S02150
A;Molecule type: protein
A;Residues: 28-35; X', 37-39; X', 41-43; X', 45-58 <W
A;Carlsson, S.R.; Fukuda, M.
R;Carlsson, S.R.; Fukuda, M.
J. Biol. Chem. 265, 20488-20495, 1990
A;Title: The polylactosaminoglycans of human lysosc A;Reference number: A23656; MUID:91056099; PMID:224
A;Accession: A23656
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J. Biol. Chem. 268, 9014-9022, 1993
A, Title: The genes of major lysosomal membrane glycoproteins, A, Title: The genes of major lysosomal membrane glycoproteins, A, Title: The genes of MacO44: MUID:93232065; PMID:8517882
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A;Molecule type: protein
A;Residues: 31-35;72-74, X',76-77;144-153;177-179,'X',181-187;215-219;255-259,'X',261
R;Carlsson, S.R.; Lycksell, P.O.; Fukuda, M.
Arch. Biochem. Biophys. 304, 65-73, 1993
A;Title: Assignment of O-glycan attachment sites to the hinge-like regions of human 1
A;Reference number: S34737; MUID:93312023; PMID:8323299
A; Map position: 13q34-13q34
C; Superfamily: lysosome-associated membrane protein
C; Keywords: glycoprotein; lysosome; transmembrane p
                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 'MARGGRVR', 40-416
A; Cross-references: GB:J03263;
                                                                                                                                                                                                                                                                                                                                                                               R;Viitala, J.; Carlsson, S.R.; Siebert, P.D.; Pukuda, M. Proc. Natl. Acad. Sci. U.S.A. 85, 3743-3747, 1988 A;Title: Molecular cloning of cDNAs encoding lamp A, a human A;Reference number: A30210; MUID:88234502; PMID:3131762 A;Accession: A30210
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A; Residues: 190-214 < CA3 >
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R;Carlsson, S.R.; Fukuda, M.
J. Biol. Chem. 264, 20526-20531, 1989
A;Title: Structure of human lysosomal membrane glycoprotein
A;Reference number: A32685; MUID:90062189; PMID:2584229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 57-71; 116-135; 215-234 < CAR>
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A;Title: Purification and characterization of human lysosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: B46044
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A; Residues: 1-416 < FUK >
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A;Accession: A31959
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A;Residues: 116-119,'X',121-128,'X',130-131,'X',133-135;163,'X',165-179,'X',181-189,'
                                                                                                                                                                                                                                                            A;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S34737
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A;Residues: 1-416 <S
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J. Biol. Chem. 263, 18920-18928, 1988
A;Title: Cloning of cDNAs encoding human lysosomal membrane
A;Reference number: A92699; MUID:89066687; PMID:3198605
                                                                                     A; Cross-references: GDB:120137; OMIM:153330
                                                                                                                          A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Date: 31-Mar-1990 #sequence revision 01-Dec-1995 #text_change 22-Jun-1999;Accession: A31959; B46044; S02150; A23656; A32655; S34737; A30210; B30210; Pukuda, M.; Viitala, J.; Matteson, J.; Carlsson, S.R.
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                                                                                                                                                                                                                                                            B3021
                                                                                                                                                                                                                                                                                       <VII>; NID:g187178;
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PMID:2243102
                                                                                                                                                                                                                                                                                          PIDN: AAA59524.1;
   protein
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F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-416/Product: lysosomal membrane glycoprotein 1 #status predicted <MAT>
F;28-381/Domain: lysosomal lumennal #status predicted <LYS>
F;382-405/Domain: transmembrane #status predicted <CYM>
F;382-405/Domain: intracellular #status predicted <CYM>
F;406-416/Domain: intracellular #status predicted <CYM>
F;36,44,83,102,106,240,248,292,321,379/Binding site: carbohydrate (Asn) (covalent) #status F;40-79,154-190,230-568,337-374/Disulfide bonds: #status experimental
F;61,75,120,129,164,180,222,227,260/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;196/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;198,199/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;206,208,210/Binding site: carbohydrate (Ser) (covalent) #status experimental
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(;Superfamily: zip protein
C;Keywords: glycoprotein; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <NAT>
F;22-500/Product: zip protein #status predicted <NAT>
F;22-470/Domain: extracellular #status predicted <TMM>
F;466-486/Domain: transmembrane #status predicted <TMM>
F;496-500/Domain: intracellular #status predicted <TMM>
                                                                                                     hypothetical protein M106.3 - Caenorhabditis elegans C;Species; Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #C;Accession: T23740 R;Palmer, S.
submitted to the EMBL Data
A;Reference number: Z19792
A;Accession: T23740
A;Status: preliminary; tran
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A;Cross-references: EMBL:X07450;
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C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 22-Jun-1999
C;Accession: S00483; A37532
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Matches
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;Residues: 1-500 <ZHA>
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ИВО J. 7, 1115-1119, 1988
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Pred. No. 40;
0; Mismatches
     from GB/EMBL/DDBJ
                                                                                 December
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A; Cross references: GB:M59936; NID:g203659; PIDN:AAA40997.1; PID:g203660 A; Cross references: GB:M59936; NID:g203659; PIDN:AAA40997.1; PID:g203660 A; Note: the authors translated the codon CAG for residue 7 as Gly and GAC C; Superfamily: gap junction protein
C; Keywords: gap junction; phosphoprotein; placenta; transmembrane protein
F;1-20/Domain: intracellular #status predicted <NTI>F;21-40/Domain: extracellular #status predicted <EE1>F;41-73/Domain: extracellular #status predicted <NTI>F;91-722/Domain: intracellular #status predicted <NTI>F;97-122/Domain: intracellular #status predicted <NTIS>F;123-159/Domain: transmembrane #status predicted <NTIS>F;123-159/Domain: transmembrane #status predicted <NTIS>F;160-184/Domain: transmembrane #status predicted <NTIS>F;160-184/Domain: transmembrane #status predicted <NTIS>F;108-270/Domain: intracellular #status predicted <NTIS>F;108-270/Domain: intracellular #status predicted <NTIS>F;108-270/Domain: transmembrane #status predicted <NTIS>F;108-270/Domain: intracellular #status predicted <NTIS>F;108-270/Domain: transmembrane #status predicted <NTIS
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J. Biol. Chem. 266, 6524-6531, 1991
J. Title: Molecular cloning and characterization of a new A;Reference number: A38737; MUID:91177912; PMID:1706719
A;Recession: A38737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap junction protein Cx31 - rat
N;Alternate names: connexin-31
C;Species: Rattus norvegicus (Norway
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A38737
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A;Residues: 1-529 <WIL>
A;Cross-references: EMBL:Z46935; PIDN:CAA87050.1; GSPDB:GN00020; CESP:M106.3
A;Experimental source: clone M106
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A;Experimental source: strain 2.4.1
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A;Title: DNA sequence analysis of the photosynthesis region
A;Reference number: Z25222; MUID:20115911; PMID:10648776
A;Accession: T50707
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R;Choudhary, M.; Kaplan,
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A; Introns: 34/1; 175/3;
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A; Residues: 1-270 < HOH>
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c92739 mus musculu
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p27859 escherichia
p34291 caenorhabdi
p49309 rhizobium m
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c94720 drosophila
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ALIGNMENTS

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his SWISS-PROT entry is copyr etween the Swiss Institute o he European Bioinformatics In se by non-profit instituti oddfied and this statement is ntities requires a license ag	AND N-GLYCOSYLATED; SOME OF THE N-GLYCANS ATTACHI TRE POLYLACTOSAMINOGLYCANS (BY SIMILARITY). TY: BELONGS TO THE LAMP FAMILY.	CATED CATED PROTEI	n L.M., Earles B.J., August J.T.; ulfide structure of mouse lysosome-associated membran 1."; Chem. 265:7419-7423(1990).	[4] DISCUFIDE BONDS. MEDITURE-90277040: PubMed=2332434:	"Isolation and sequencing of a CDNA clone encoding lysosomal membrane glycoprotein mouse LAMP-1. Sequence similarity to proteins bearing onco-differentiation antigens." J. Biol. Chem. 263:8754-8758(1988).	25-406 FROM N.A.; AND PARTIAL SEQUENCE 43732; PubMed=3379044;	[2] SEQUENCE FROM N.A. Heffernan M., Yousefi S., Dennis J.W.; Submitted (FEB-1990) to the EMBL/GenBank/DDBJ databases.	Helenius A.; "Characterization and cloning of lgp110, a lysosomal membrane glycoprotein from mouse and rat cells."; "Characterization from mouse and rate cells."	LAMMET OK LAMMET. Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. MCBI TaxID=10090; [1]	01-OCT-1989 (Rel. 12, Created) 01-OCT-1999 (Rel. 15, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) 10-NOV-1997 (Rel. 35, Last annotation update) 11-10-11-12-12-13-13-13-13-13-13-13-13-13-13-13-13-13-	1 OUSE MP1_MOUSE

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Pfam; PF01299; Lamp; 1.
PRNNTS; PR00336; LYSASSOCTDMP.
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Transmembrane; Glycoprotein; Lysosome; Signal.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and sequencing of a cDNA clone encoding 107 kDa sialoglycoprotein in rat liver lysosomal membranes."; FEBS Lett. 244:351-356(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Himeno M., Noguchi Y.,
Sakaki Y., Kato K.;
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Proc. Natl. Acad
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SEQUENCE FROM N.A.
MEDLINE=89017240; PubMed=3174652;
Howe C.L., Granger B.L., Hull M.,
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EMBL; X14765; CAA32873.1; -.
EMBL; U75406; AAB19108.1; -.
FIR; A30200; A30200.
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PROSITE; PS00310; LAMP 1; 2.
PROSITE; PS00311; LAMP 2; 1.
Transmembrane; Glycoprotein; L
SIGNAL 1
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PTM: O- AND N-GLYCOSYLATED; SOME OF THE LAMP-1 ARE POLYLACTOSAMINOGLYCANS (BY SIMILARITY: BELONGS TO THE LAMP FAMILY.
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            PubMed=2920835;
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P11279;

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01-JAN-1990 (Rel. 13, Last seq

16-OCT-2001 (Rel. 40, Last ann

Lysosome-associated membrane g

(CD107a antigen).
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Hildreth J.
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MEDLINE=90062189;
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Arch. Biochem.
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Hildreth J.E.K., August J.T.;
"Purification and characterization
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      Fukuda
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Rainton D.
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                                   PubMed=2584229;
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sosomal membrane glycoproteins,
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         MIM; 15330; -.
GG; GG:0005887; C:integral to plasma membrane; TAG; GG:0005764; C:lysosome; TAS.
GG; GG:0005764; C:membrane fraction; TAS.
Interpro; IPR002000; Lamp.
Pfam; PF01299; Lamp; 1.
PFAM; PF01299; Lamp; 1; 2.
PROSITE; PS00316; LYSASSOCTDMP.
PROSITE; PS00311; LAMP 2; 1.
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Carlsson S.R., Fukuda m.;
Carlsson S.R., Fukuda m.;
"The polylactosaminoglycans of human ly lamp-1 and lamp-2. Localization on the lamp-1 and Lamp-2. 265:20488-20495(1990)."
                                                                                                                                                                                                                                                                                                                                                                                          Carlsson S.R., Lycksell P.-O., Fukuda M.;

"Assignment of O-glycan attachment sites to the hir
human lysosomal membrane glycoproteins lamp-1 and l
Arch. Biochem. Biophys. 304:65-73(1993).

-i- FUNCTION: PRESENTS CARBOHYDRATE LIGANDS TO SELF
-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- SUBCELLULAR LOCATION: Type I membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure of human lysosomal membrane glycoprotein 1. Assignment of disulfide bonds and visualization of its domain arrangement."; J. Biol. Chem. 264:20526-20531(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYLACTOSAMINOGLYCANS
                                                                                                                                                                                                                         MEMBRANE.

PTM: O- AND N-GLYCOSYLATED; SOME OF THE 18 N-GLYCANS I
LAMP-1 ARE POLYLACTOSAMINOGLYCANS.

SIMILARITY: BELONGS TO THE LAMP FAMILY.

DATABASE: NAME=PROW; NOTE=CD guide CD107a entry;

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd107a.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=2243102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lysosomal'membrane glycoproteins peptide backbones.";
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EMBL; J04182; AAA60382.1; EMBL; J03263; AAA59324.1; PIR; A31959; A31959
GlycoSulteDB; P11279; Genew; HGNC:6499; LAMP1.

N-LINKED (GLCNAC...).
N-LINKED (GLCNAC...)
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(POLYLACTOSAMINOGLYCAN).
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MEDLINE=88296414; PubMed=3402433;

Zhao D.-B., Code S., Jaehnig F., Haller J., Jaeckle H.;

Zhpper encodes a putative integral membrane protein recormal axon patterning during Drosophila neurogenesis."

EMBO J. 7:1115-1119(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Haxpoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TZIP DROME STANDARD; PRT; 488 AA.
P10379; Q96084; Q98087;
01-MAR-1989 (Rel. 10, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
UZIP OR ZIP OR CG3533.
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UNZIPPED PROTEIN.
EXTRACELLULAR (POTENTIAL
POTENTIAL.
CYTOPLASMIC (POTENTIAL)

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Transmembrane; Signal

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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Ra Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Ra Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kunp D., Lai Z.,
Ra Lasko P., Lei Y., Levisky A.A., Li J., Li Z., Liang Y., Lin X.,
Ra Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Ra Hiu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Ra McIntosh T.C., McLeod M.P., McPherson D.L.,
Ra Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Ra Melson D.R., Nelson K.A., Nixon K., Nisskern D.R., Pacleb J.M.,
Ra Melson D.R., Nelson K.A., Nixon K., Nisskern D.R., Pacleb J.M.,
Ra Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Ra Shier E., Spradling A.C., Stappeon M., Skupski M.P., Smith T.,
Ra Spier E., Spradling A.C., Stappeton M., Strong R., Sun E.,
Ra Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
Ra Shue B.C., Salan D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Ra Milliams S.M., Woodage T., Worley K.C., Mu D., Yang S., Yao Q.A.,
Ra Meng X.H., Zhong F.N., Zhan M., Zhang G., Zhao Q., Zheng L.,
Ra Jheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
Ra Globs R.A., Myers E.W., Rubin G.M., Venter J.,
C., Schence 287:2185-2195(2000)
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STRAIN=Berkeley; TISSUE=Embryo;
STRAIN=Berkeley; TISSUE=Embryo;
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use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for com-
entities requires a license agreement (See http://www.isb-sib.ch/an
or send an email to license@isb-sib.ch).
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S
smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.
EMBL; X07450; CAA30332.1; -.
EMBL; AE003465; AAF47312.2;
EMBL; AY052139; AAK93563.1;
PIR; S00483; EFFF.
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                                                                                                                                                                                                                                                                                                                                                    noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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Rubin G.M.,
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RP SEQUENCE FROM N.A.

RC TISSUE-Urinary bladder;
RX MEDLINE=22388257; PubMed=12477932;
RX MEDLINE=22388257; PubMed=12477932;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shendefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Clasavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Clasavant T.L., Scheetz T.E.,
RA Stapleton M., Joquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bonask S.A., McEwan P.J., McKernan K.J., Marsanon R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Hotting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
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Best Local
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TISSUE=Placenta;
MEDLINE=98369649; PubMed=9704026;
Menzel K., Manthey D., Willecke K., Grzeschik K.-H., Traub
Wenzel K., Manthey D., Traub
Wenzel K., Manthey D., Willecke K., Grzeschik K.-H., Traub
Wenzel K., Manthey D., Willecke K., Grzeschik K.-H., Traub
Wenzel K., Manthey D., Willecke K., Grzeschik K.-H., Traub
Wenzel K., Manthey D., Willecke K., Grzeschik K.-H., Traub
Wenzel K., Manthey D., Willecke K., Grzeschik K.-H., Traub
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Wenzel K., Manthey D., Willecke K., Grzeschik K.-H., Traub
Wenzel K., Manthey D., Willecke K., Grzeschik K.-H., Traub
Wenzel K., Walthey M., Willecke K., Willeck
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SEQUENCE
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15-SEP-2003
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MEDLINE=99057343; PubMed=9843209;

MICHARD G., Smith L.E., Bailey R.A., Itin P., Hohl D.,

Epstein E.H. Jr., Digiovanna J.J., Compton J.G., Bale S.J.;

"Mutations in the human connexin gene GJB3 cause erythrokeratodermia variabilis.";

Variabilis.";

Variabilis.";
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"Molecular cloning of h
Submitted (FEB-1999) to
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Mammalia; Eutheria;
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(Rel. 37, Last sequence upo
(Rel. 42, Last annotation)
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human connexin 31 and 31.1 genes.";
to the EMBL/GenBank/DDBJ databases.
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; 584E93D9012A2BE7 «
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EMBL; AJ004856; CAA06165.1; -.
EMBL; AF052692; AAD11816.1; -.
EMBL; AL121988; CAB90269.1; -.
EMBL; AF099730; AAC95471.1; -.
EMBL; BC012918; AAH12918.1; -.
PIR; JE0274; JE0274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hum. Genet. 106:321-329(2000).

Hum. Genet. 106:321-329(2000).

PUNCTION: One gap junction consists of a cluster of closely packe pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell.

SUBCELLULAR LOCATION: Integral membrane protein.

IDISEASE: Defects in GUBB are a cause of erythrokeratedermia variabilis (EKV) [MIM:133200], an autosomal dominant disease characterized by 2 morphologic features: transient figurate red patches and localized or generalized hyperkeratosis.

DISEASE: Defects in GUBB are a cause of autosomal dominant non-syndromic sensorineural deafness type 2 (DFNA2) [MIM:600101].

SUBDILARITY: BELONGS TO THE CONNEXIN FAMILY. BETA-TYPE (GROUP I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20256220; PubMed=10798362; Richard G., Brown N., Smith L.E., Mackie R.M., Bale S.J., Uitto J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20062991; PubMed=10594760; Wilgoss A., Leigh I.M., Barnes M.R., Dopping-Hepenstal P., Wilgoss A., Leigh I.M., Kennedy C.T., Kelsell D.P., Eady R.A.J., Walter J.M., Kennedy C.T., Kelsell D.P., "Identification of a novel mutation R42P in the gap junction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99057344; PubMed=9843210;
Xia J.-H., Liu C.-Y., Tang B.S., Pan Q.,
Zhang B.R., Xie W., Hu D.X., Zheng D., S
Yu K.P., Liao X.D., Feng Y., Yang Y.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci
[6]
VARIANT DFNA2 LYS-183
                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for com-
entities requires a license agreement (See http://www.isb-sib.ch/ar
or send an email to license@isb-sib.ch).
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MEDLINE=20062991; I
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                            InterPro; IPR000500; Connexin.
Pfam; PF00020; connexin; 1.
PRINTS; PR00206; CONNEXIN.
SMART; SM00037; CNX; 1.
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                                                                                                GO; GO:0007154;
                                                                                                                                               MIM; 603324; -
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DATABASE: NAME=Connexin-deafness homepage;

WWM="http://www.crg.es/deafness/".

DATABASE: NAME=Hereditary hearing loss hom
                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE=Gene page;
WWW="http://www.uia.ac.be/dnalab/hhh/".
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1. Acad. Sci. U.S.A. 9
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                                                                                             P:cell communication;
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impairment.";
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., Shi X.L., Wang D.A., Xia
F., Xiao J.Y., Xie D.H.,
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SMART; SM00037; CNX; 1.
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Matches 6
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use by non-profit institutes. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restr
                                                                                                           -!- FUNCTION: One gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell.
-!- SUBUNIT: A connexon is composed of a hexamer of connexins.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=92347372; PubMed=1322300;

Hennemann H., Schwarz H.J., Willecke K.;

"Characterization of gap junction genes expressed in F9 embryonic carcinoma cells: molecular cloning of mouse connexin31 and -45 carcinoma cells: molecular cloning of mouse connexin31 and -45
                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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GJB3 OR CXN-31
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1.beta-3 protein (Connexin 31) (
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Pred. No. 18;
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/FTId=VAR_002150.
E46D36E5835646A4 CRC64;
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P25305;
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                                                                                                    This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and to
                                                                                                                                                                                                                                                            MEDLINE=91177912; PubMed=1706719;
Hoh J.H., John S.A., Revel J.-P.;
"Molecular cloning and characterization of a new member of the gap junction gene family, connexin-31.";
J. Biol. Chem. 266:6524-6531(1991).
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MGD; MGI:95721; Gjb3.
InterPro; IPR000500; Connexin.
       InterPro; IPR000500; Con
Pfam; PF00029; connexin;
PRINTS; PR00206; CONNEXI
                                          EMBL; M59936; AAA40997.1; -. PIR; A38737; A38737.
                                                                              entities requires a license agreement (S or send an email to license@isb~sib.ch).
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                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
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16-OCT-2001
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                                                                                                                                                                                     pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring ce SUBUNIT: A connexon is composed of a hexamer of connexins. SUBCELLULAR LOCATION: Integral membrane protein. SUBCELLULAR INCATION: THE CONNEXIN FAMILY. BETA-TYPE (GROUP SIMILARITY: BELONGS TO THE CONNEXIN FAMILY.
                                                                                                                                                                                                                                                   FUNCTION: One gap junction consists of a cluster of closely packed
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POTENTIAL.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

POTENTIAL.
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Pred. No.
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CYTOPLASMIC (POTENTIAL)
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Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                  There are no restrictions 
ng as its content is in
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CONNEXIN

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W MEDLINE-92381038; pubMed=1512260;

A Hennemann H., Dahl E., White J.B., Schwarz H.J., Lalley P.A.,

A Chang S., Nicholson B.J., Willecke K.;

Chang S., Nicholson B.J., Willecke K.;

Two gap junction genes, connexin 31.1 and 30.3, are closely linked or mouse chromosome 4 and preferentially expressed in skin.";

J. Biol. Chem. 267:17225-17233 (1992).

C -i- FUNCTION: One gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell.

C -i- SUBCINIT: A connexon is composed of a hexamer of connexins.

C -i- SUBCILULAR LOCATION: Integral membrane protein.

C -i- SINGCILULAR LOCATION: Integral membrane protein.

C -i- SINGLELULAR SECONGS TO THE CONNEXIN FAMILY. BETA-TYPE (GROUP I)

C SUBFRAMILY: BELONGS TO THE CONNEXIN FAMILY. BETA-TYPE (GROUP I)
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Best Local
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Q02739;
Q1-FEB-1994
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01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2093 (Rel. 41, Last amotation update)
28-FEB-2093 (Rel. 41, Last amotation update)
Gap junction beta-5 protein (Connexin 31.1)
GJBS OR CXN-31.1.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Ver
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PROSITE; PS004
Gap junction;
DOMAIN
PROSITE; PS00407; CONNEXINS 1; 1. PROSITE; PS00408; CONNEXINS 2; 1. Gap junction; Transmembrane. CYTO DOMAIN 1 20 CYTO
                                                                                              InterPro; IPR000500; Conne:
Pfam; PF00029; connexin; 1
PRINTS; PR00206; CONNEXIN.
SMART; SM00037; CNX; 1.
                                                                                                                                                                  EMBL; M91236; AAA37426.1; -.
EMBL; M91442; AAA37427.1; -.
PIR; B43433; B43433.
MGD; MGI:95723; Gjb5.
InterPro; IPR000500; Connexin.
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6; Conserv
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01-DEC-1992
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                                                                                                                                                                                                                                          Zo-rab-2003 (Rel. 41, Last annotation update)
Gap junction beta-5 procein (Connexin 31.1) (
GJB5 OR CXN-31.1.
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SEQUENCE
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                                                                                                                       EMBL; M76533; AAB38538.1; -. PIR; D42053; D42053. Connexin. InterPro; IPR000500; Connexin.
                                                                                                                                                                                                                                                                                                                                                MEDLINE=92112940; PubMed=1370487;
Haefliger J.-A., Bruzzone R., Jen
                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                         PROSITE; PS00407; CONNEXINS_1; PROSITE; PS00408; CONNEXINS_2;
                                                                                             SMART; SM00037; CNX;
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                                                                                                               PF00029; connexin;
                                                                                                                                                                                                                                                                                                                and N.G., Paul D.L.;
novel members of the connexin family of
novel members are expression, and chromosome
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                                                                                                     PR00206; CONNEXIN.
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
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Pred. No.
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CYTOPLASMIC (POTENTIAL)
POTENTIAL.
EXTRACELLULAR (POTENTIA
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EXTRACELLULAR (POTENTIAL)
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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mapping.";
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RX MEDILINE=2238057; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmen K.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmen K.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmen K.A., Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Dudin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Kocewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Robriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Robriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Batterfield Y.S.N. Schmutz J., Warrs M.A.;

"Generation and initial analysis of more than 15,000 full-length

RT manush and mouse cDNA sequences",

Batterfield Y.S.N. Schmutz J., Warrs M.A.;

"Generation and initial analysis of more than 15,000 full-length

RT more sequences ",

Batterfield Y.S.N. Schmutz J., Warrs M.A.;

"Generation and initial analysis of more than 15,000 full-length

RT more sequences ",

Batterfield Y.S.N. Schmutz J., Warr
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Best Local
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095377; Q9UPA3;
15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
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Xia J.-H.
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Richard G., Smith L.E., Bailey R.A., Itin P., Hohl D.,
Epstein B.H. Jr., DiGiovanna J.J., Compton J.G., Bale S.J.;
"Mutations in the human connexin gene GJB3 cause erythrokeratodermia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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connexin 31 and 31.1.";
EMBL/GenBank/DDBJ databases.
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CYTOPLASMIC (POTENTIAL).
7753FC96909015CE CRC64;
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Q61001; Q9JHQ6;
Q1-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence upon
15-SEP-2003 (Rel. 42, Last annotation
                                                                                                                                   A/GBI '192 FROM N.A., AND SECTION STRUCTURE 1992 FROM N.A., AND SECTION SEQUENCE OF 1-92 FROM N.A., AND SECTION SECTION SERVICE OF 1-92 FROM N.A., Timpl R., Sasaki T.;

MEDIINE-21818471, PubMedeil1829758;

MEDIINE-21818471, PubMedeil
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EMBL; AF052693; AAD18005.1;
EMBL; AL121988; CAB90271.1;
EMBL; BC004379; AAH04379.1;
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STRAIN=C57BL/6 X CBA; TISSUE=Lung; MEDLINE=96081906; PubMed=7499364; Miner J.H., Lewis R.M., Sanes I.R.; "Molecular cloning of a novel laminin expression in adult mouse tissues."; J. Biol. Chem. 270:28523-28526(1995).
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Mammalia; Eutheria;
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RP REVISIONS.

RA Miner J.H., Lewis R.M., Sanes J.R.;

RA Miner J.H., Lewis R.M., Sanes J.R.;

RI Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin conformation of cells into tissues during embryonic development by interacting converted to the extracellular matrix components.

CC -!- FUNCTION: ALPHA-5 CHAIN MAY BE THE MAJOR LAMINIAE.

CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three confiderent bolypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each
        HSSP; P02468; ITLE:

MGD; MGI:105382; Lama5.

GO; GO:005504; C:bassement membrane; IDA.

GO; GO:005044; P:lung development; IMP.

InterPro; IPR006209; EGF like.

InterPro; IPR00034; Laminin_EGF.

InterPro; IPR00193; Laminin_G.

InterPro; IPR00193; Laminin_G.

InterPro; IPR00193; Laminin_G.

Pfam; PF00052; laminin_G; 1.

Pfam; PF00053; laminin_Merm; 1.

Pfam; PF00053; laminin_Merm; 1.

Pfam; PF00055; laminin_G; 2.

Pfam; PF00055; laminin_B; 1.

PF00m; PD002082; Lam NC; 1.

PRODom; PD002082; Lam NC; 1.

PRODom; PD002082; LamG; 5.

SMART; SM00281; LamG; 5.

SMART; SM00281; LamG; 5.

SMART; SM00282; LamG; 5.

SMART; SM00283; LamMin; 1.

PROSITE; PS01186; EGF-1; 19.

PROSITE; PS01248; LamMin; 1.

PROSITE; PS01248; LamMin; 5.

SMART; SM00283; LamG; 1.

SMART; SM00283; LamG; 1.

SMART; SM00284; LamMin; EGF-LII

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EMBL; U37501; AAC53430.1;
PIR; T10053; T10053.
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                                           This SWISS-PROT entry is copyright. It is produced through a clotween the Swiss Institute of Bioinformatics and the EMBL the Buropean Bioinformatice Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                 PubMed=9169869,

Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,

Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,

Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,

Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,

Lin D., Mosedale D., Nakahara K., Namath A., Norgren R.,

Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,

Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome V.",

Nature 387:78-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces
NCBI_TaxID=4932;
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(Rel. 42, Last annotation update)
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Best Local :
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Bailey M.J.A., Koronakis V., Schmoll T., Hughes C.;
"Escherichia coli HlyT protein, a transcriptional activator of haemolysin synthesis and secretion, is encoded by the rfaH (sfrB) locus required for expression of sex factor and lipopolysaccharide genes.";
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16-OCT-2001 (Rel. 40, Last sequence up
28-PEB-2003 (Rel. 41, Last annotation
Deoxyribonuclease tatD (EC 3.1.21.-) (TATD OR MITC OR B3840/B3841.
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SGD; S0000923; YERIZIW.

Hypothetical protein.

SEQUENCE 114 AA; 12941 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 Sargent F., Bogsch E.G., Stanley N.R. Berks B.C., Palmer T.; Beerlapping functions of components protein export pathway."; EMBO J. 17:3640-3650(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=92358234; PubMed=1379743;
MEDLINE=92358234; PubMett G. III, Burland V.D., B
Daniels D.L., Plunkett G. III, Burland V.D., B
"Analysis of the Escherichia coll genome: DNA
from 84.5 to 86.5 minutes";
Science 257:771-778(1992).
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Enterobacteriaceae; Escherichia.
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EMBL; AE000459; AAC76844.1; ALT FRAME.
EMBL; X65013; -; NOT ANNOTATED CDS.
EMBL; AJ005830; CAA06727.1; ALT INIT.
ECOGene; EG11481; tatD.
ECOGENE; EG11481; tatD.
InterPro; IPR001130; TatD_Dnase.
Pfam; PF01026; TatD DNase; 1.
PROSITE; PS01037; TATD_2; 1.
PROSITE; PS010391; TATD_2; 1.
PROSITE; PS010391; TATD_3; 1.
                                                                                               EMBL; 232679; CAA83596.1; -
PIR; C88571; C88571; WormPep; C0585.3; CE17369.
Hypothetical protein.
SEQUENCE 401 AA; 43472 M
                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ethe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Durbin R.; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 260 AA; 28974 MW; C18FB5269849746F CR
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                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0035; HTHGNTR.
SMART; SM00345; HTH GNTR; 1.
PROSITE; PS00043; HTH GNTR FAMILY; 1.
Transcription regulation; DNA-binding; Transferase; Aminotransferase;
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Rossbach S., Kulpa D.A., Rossbach U., de Bruijn F.J.;
Rossbach s., Kulpa D.A., Rossbach U., de Bruijn F.J.;
Wolecular and genetic characterization of the rhizopine catabolism (mocABRC) genes of Rhizobium meliloti L5-30.";
Mol. Gen. Genet. 245:11-24(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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(zopine catabolism regulatory protein
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Q96140 homo sapien
Q9brd2 homo sapien
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adont de te	מרשלי לכיים	arabidor	photorhak	μ,	clostridiu	agro	synechocys	oryza sa	taphyloco	irofilar	bacillus	leptosp	O29728 archaeoglob	brachydani	ac	Q8cv82 oceanobacil	킖	ă	Q8qgj5 fugu rubrip	bacterioph	Q9rff6 rhodobacter	Q8dsr6 streptococc	P97705 rattus norv	Q9w4v1 drosophila	ìrosophil	O	œ	Q8irv2 drosophila	w

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Q9X494;
01-NOV-1999
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Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
"Differential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-activating lipopoptide of Mycoplasma fermentans.";
Interpromun. 67:760-771(1999).

EMBL; AF100324; AAD25734.1; -.
EMBL; AF100324; AAD25734.1; -.
Interpro; IFR000578; UpF0011.
Interpro; IFR000578; UpF0011.
Pfam; PF00590; TF methylase; 1.
Pfam; PF00590; TF methylase; 1.
PROSITE; P801296; UPF0011; 1.
PROSITE; P801296; UPF0011; 1.
PROSITE; P801296; UPF0011; 1.
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01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2003 (TrEMBLrel. 23,
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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    112
                                                                           1 GVNAXSSAF 9
                                                                                                                                                      Similarity 7; Conserv
    GVNAAISAF 120
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                                                                                                                                                          Conservative
                                                                                                                                                                                           82.1%; Score 32; DB 77.8%; Pred. No. 29;
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01-OCT-2001
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01-JAN-1998
01-MAR-2002
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MEDLINE-2135/209; PubMed=11463916;
Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin.A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Umayam L.A., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lancet 357:1225-1240(2001).

EMBL; AF001782; AAB63265.1;

EMBL; AP003364; BAB58199.1;

EMBL; AP003135; BAB43124.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutenni-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Sekimizu K., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Mhole genome sequencing of meticillin-resistant Staphylococcus
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=S. aureus; STRAIN=SA502A; MEDLINE=97342847; PubMed=9197262; Ji G., Beavis R., Novick R.P.; "Bacterial interference caused by Science 276:2027-2030(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGRD (AGRD protein).
AGRD OR SAV2037 OR SA1842.1 OR SAS066.
Staphylococcus aureus (strain Mu50 / ATC)
Staphylococcus aureus (strain N315), and
                                                                                                                                           Streptococcus.
NCBI_TaxID=1313;
                                                                                                                                                                                                    Hypothetical SP1652.
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                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                         Bacteria, Firmicutes,
                                                                                                                                                                                      Streptococcus pneumoniae
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1 (TrEMBLrel. 19,
al protein SP1652.
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Q8CYG6;
01-MAR-2003
01-MAR-2003
01-MAR-2003
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Q9CC58;
01-JUN-2001
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MEDLINE=21429245; PubMed=11544234;
Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett & Hoskins J., Alborn W.E. Jr., Fritz L., Fu D.-J., Fuller W., Geringes DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringes Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Iu J., Matsushima P., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Mundy C.W., Nicas T.I., McArren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., 20ck C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 183:5709-5717(2001).

EMBL; AE008518; AAL00300.1; -.

Hypothetical protein; Complete pro-

SEQUENCE 924 AA; 102967 MW; 19
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Pfam; PF02887; DUF214; 2.
Hypothetical protein; Complete
SEQUENCE 924 AA; 102997 MW;
                                                                   Mycobacterium leprae.
Bacteria; Actinobacteridae; Actinomycetales;
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01-OCT-2001
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TIGR; SP1652; -
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Science 293:498-506(2001)
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Corynebacterineae; Mycobacteriaceae; Mycobacterium NCBI_TaxID=1769;
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102967 MW:
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Lactobacillales;
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Last ann
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2; Mismatches
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192383CF91548592
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C75B27650ED9C65F CRC64;
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Geringer C.,
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Matches
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C.; Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.;
"Maccional Control of the Cont
                                                                    laboratory strains.";
Submitted (APR-2001) to the
EMBL; AL021246; CAA16045.1;
EMBL; AE007091; AAK46843.1;
TIGR; MT2543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98295987; PubMed=9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Besham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O53195 PRELIMINARY; PRT; 167 AA.
O53195; PTEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv2468c
RV2468C OR MTV008.24C OR MTZ543.
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SEQUENCE F
STRAIN=TN;
                                                                                                                                                                                                                                                                                                                                     STRAIN=CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Kolonay J.F., Nelson W.C., Umayam J., Khouri H., Gill J., Mikula Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=H37RV;
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EMBL; AL583921; CAC31636.1; -.
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NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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        Rv2468c;
protein;
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16842 MW;
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77
Complete
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Strausberg R.;
Submitted (APR-2001) to the EMBI
EMBL; BC006785; AAH06785.1; -.
InterPro; IPR002000; Lamp.
Pfam; PF002299; Lamp; 1.
PRINTS; PR00336; LYSASSOCTDMP.
PROSITE; PS00310; LAMP_1; 1.
                                                                                                                                                                                                                                                                               Q922T9
Q922T9;
Q1-DEC-2001
01-DEC-2001
01-MAR-2003
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Q9X7B5;
01-NOV-1999
01-NOV-1999
01-DEC-2001
                                                                                                                                                                                                                                        Similar to lysosomal Mus musculus (Mouse)
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James K.D., Parkhill
Submitted (MAR-1999)
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Bacteria; Actinobacteria;
Corynebacterineae; Mycobac
MCBI_TaxID=1769;
                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 1
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                                                                                                                                          EQUENCE FROM N.A.
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0; Mismatches
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Strausberg R.;
Submitted (MAY-2001) to the
EMBL; BC007845; AAH07845.1;
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01-OCT-2002 (TrEMBLrel. 22, C
01-OCT-2002 (TrEMBLrel. 22, I
01-MAR-2003 (TrEMBLrel. 23, I
Cytochrome cridase subunit
                                                                                     SEQUENCE FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000298; CytC_oxdse_III.
ProDom; PD000382; CytC_oxdse_III; 1.
PROSITE; PS50253; COX3; 1.
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-!- FUNCTION: SUBUNITS I, II AND III FORM THE FUNCTIONAL ENZYME COMPLEX (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 F C + 2 H(2)O.
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Cyclophyllidea; Taeniidae;
CNCBI_TaxID=6204;
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NA; 24442 MW; 4E59E1E14E876C5E CRC64;
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Primates;
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t 3 (EC 1.9.3.1) (Cytochrome
                              EMBL/GenBank/DDBJ databases
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Pred. No.
                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Best Local S
Matches
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Best Local S
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Pfam; PF01299; Lamp; 1.
PRINTS; PR00336; LYSASSOCTDMP.
PROSITE; PR003310; LAMP 1; 1.
PROSITE; PS00311; LAMP 2; 1.
                                                                                                                                                                                                                                                                                                             Q9NP13;
Q9NP13;
01-OCT-2000
01-OCT-2000
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, BC006345, AAH06345.1;
InterPro; IPR002000; Lamp.
Pfam; PF01299; Lamp; 1.
PRINTS; PR00220
SEQUENCE FROM N.A.
TISSUB-Placenta;
TISSUB-Placenta;
MEDLINE-89066687; PubMed-3198605;
Fukuda M., Viitala J., Matteson J., Carlsson S.R.;
Fukuda M., Viitala J., Matteson J., Carlsson S.R.;
"Cloning of cDNAs encoding human lysosomal membrane glycoproteins,
"Cloning of cDNAs encoding human lysosomal membrane glycoproteins,
"Cloning of cDNAs encoding human lysosomal membrane glycoproteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0336; LYSASSOCTDMP.
PROSITE; PS00310; LAMP 1; 1.
PROSITE; PS00311; LAMP 2; 1.
NON TER 1
SEQUENCE 311 AA; 33713 MW;
                                                                                                                                                                     NCBI_
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Similar to lysosomal-associated membrane protein 1
                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                    LAMP1.
                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 25, Last annotation update)
Lysosomal-associated membrane glycoprotein-1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
Strausberg R.;
Submitted (APR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                            _TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                Chordata;
Primates;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 90;
1; Mismatches
                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
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885
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2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
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RESULT Q8VH34 ID Q8VH34 ID Q8 PT 011 DT 011 
                  RESULT
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EMBL; L08576; AAF66141.1; JOINED.
EMBL; L08577; AAF66141.1; JOINED.
EMBL; L08578; AAF66141.1; JOINED.
EMBL; L08578; AAF66141.1; JOINED.
EMBL; L08580; AAF66141.1; JOINED.
EMBL; L08581; AAF66141.1; JOINED.
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Q8VH34;
01-MAR-2002
01-MAR-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (DEC 2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AY069968; AAL58070.1; -.

INTERPRED I IPRO02000; Lamp.

Pfam; PF0129; Lamp; 1.

PRINTS; PR00336; LYSASSOCTDMP.

PROSITE; PS00310; LAMP_1; 2.

PROSITE; PS00311; LAMP_2; 1.

SEQUENCE 406 AA; 43879 MW; C1BD373548ADFA85 CRC64;
     Q9DC13 PRELIMINARY;
Q9DC13;
Q1-JUN-2001 (TremBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE=9332065; PubMed=8517882; Sawada R., Jardine K.A., Fukuda M.; Sawada R., Jardine K.A., Fukuda M.; "The genes of major lysosomal membrane glycoproteins, lamp-1 and lamp-2.5'.flanking sequence of lamp-2 gene and comparison of exon organization in two genes [published erratum appears in J Biol Chem 1993 Jun 15;268(17):13010).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ono K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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NON TER 1 1 1

SEQUENCE 355 AA; 38358 MW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00336; LYSASSOCTDMP
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                                                                                                                                                                                                                                                                                         Similarity 6; Conserv
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                                                                                                                                                                                            GMNASSSLF
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                                                                                                                                                                                                                                                                                            Conservative
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66.7%;
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66.7%;
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                                                                                                                                                                                                                                                                               Score 30; DB 1
Pred. No. 1.5e-
1; Mismatches
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1. No. 1.5e+02;
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Strausberg R.;
Strausberg R.;
Strausberg R.;
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Submitted (JAN-2002) to the EMBI EMBL; BC021288, AAH21288, 1;
InterPro; IPR02000; Lamp.
Pfam; PF01299; Lamp; 1.
PRINTS; PR00336; LYSASSOCTDMP.
PROSITE; PS00310; LAMP_1; 2.
PROSITE; PS00311; LAMP_2; 1.
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Q8WU33;
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                                                                                                                                                                                                       ISSUE=Pancreas;
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Query Match
Best Local Similarity
6; Conserve
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RC STRAIN=C57BL/6J; TISSUE=Lung;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kadachi J., Fukuda S.,

Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Asito Y., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Asito Y., Matsuda T., Gissi C., King B., Kochiwa H.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Oyackenbugh J.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Oyackenbugh J.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Oyackenbugh J.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Oyackenbugh J.,

RA Kuchl P., Lewis S., Hatsuo M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Whitsiki S.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Pfam; PR01299; Lamp; 1.
Pfam; PR00336; LYSASSOCTDMP.
PROSITE; PR00310; LAMP 1; 2.
PROSITE; PS00311; LAMP 2; 1.
SEQUENCE 407 AA; 43936 MW; 6
                           Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; P.
                                                                                                                                                   01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001).
EMBL; AK004637; BAB23428.1;
MGD; MGI:96745; Lamp1.
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Mammalia; Eutheria; Rodentia;
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NCBI_TaxID=9606;
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Last sequence update)
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Pred. No. 1.5e+02;
                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Sciurognathi; Muridae;
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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      protein search, using
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length: 2000000000
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Match Length
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
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                US-09-339-511-7

US-08-839-511-1

US-08-83-476C-6

US-08-861-476C-6

US-08-073-807A-17

US-08-073-807A-18

US-08-073-807A-18

US-08-073-807A-18

US-09-331-784A-26

US-09-339-511-6

US-09-339-511-6

US-09-339-511-6

US-09-339-511-6

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Sequence 7, Appli
Sequence 3, Appli
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Sequence 17, Appli
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28 71.8 533 6 5206152-2 27 69.2 248 3 US-09-111-470-2 28 69.2 248 3 US-09-750-145A-20 29 69.2 248 3 US-08-750-145A-20 29 69.2 248 3 US-08-750-145A-20 20 69.2 248 3 US-08-750-145A-20 21 69.2 248 3 US-08-750-24 22 69.2 248 3 US-09-477-090-24 23 69.2 248 4 US-09-724-510-2 24 69.2 319 4 US-09-724-510-2 25 69.2 319 4 US-09-723-216-2 26 69.2 319 4 US-09-723-216-2 27 69.2 319 4 US-09-723-216-2 28 69.2 319 4 US-09-723-216-2 29 69.2 319 4 US-09-723-216-2 20 69.2 319 4 US-09-675-227-2 21 69.2 343 4 US-09-967-908A-8 22 69.2 363 4 US-09-967-908A-6 23 69.2 363 4 US-09-967-908A-6 24 69.2 363 1 US-08-186-833-2 25 69.2 362 1 US-08-186-833-2 26 69.2 363 1 US-09-521-780-5 27 69.2 579 4 US-09-521-780-5 28 69.2 579 4 US-09-521-780-5 29 69.2 634 4 US-09-328-352-4627 29 69.2 758 1 US-08-258-188-2 20 69.2 758 1 US-08-258-188-2
1.8 533 6 5206152-2 Patent No. 520615 9.2 243 3 US-09-111-470-2 Sequence 20, Appl 9.2 248 3 US-09-5-698A-24 Sequence 24, Appl 9.2 248 3 US-09-5-698A-24 Sequence 24, Appl 9.2 248 3 US-09-417-090-24 Sequence 24, Appl 9.2 248 3 US-09-417-090-24 Sequence 24, Appl 9.2 248 3 US-09-724-510-2 Sequence 2, Appl 9.2 319 4 US-09-724-510-2 Sequence 2, Appl 9.2 319 4 US-09-723-216-2 Sequence 2, Appl 9.2 319 4 US-09-723-216-2 Sequence 2, Appl 9.2 319 4 US-09-675-227-2 Sequence 2, Appl 9.2 319 4 US-09-675-908A-8 Sequence 10, Appl 9.2 363 4 US-09-967-908A-6 Sequence 4, Appl 9.2 363 4 US-09-967-908A-6 Sequence 6, Appl 9.2 382 1 US-09-121-780-5 Sequence 2, Appl 9.2 382 1 US-09-521-780-5 Sequence 4, Appl 9.2 579 4 US-09-521-780-5 Sequence 4, Appl 9.2 579 4 US-09-521-780-5 Sequence 4627, Appl 9.2 758 1 US-08-258-188-2 Sequence 2, Appl
33 6 5206152-2 Patent No. 520615 3 3 US-09-111-470-2 \$ Sequence 20, Appl 48 3 US-08-975-698A-24 \$ US-09-975-698A-24 \$ US-09-727-578-24 \$ US-09-727-578-24 \$ US-09-727-578-24 \$ US-09-724-510-2 \$ US-09-724-510-2 \$ US-09-724-510-2 \$ Sequence 24, Appl 4 US-09-724-510-2 \$ Sequence 2, Appl 19 4 US-09-723-216-2 \$ Sequence 2, Appl 19 4 US-09-675-207-2 \$ Sequence 2, Appl 4 US-09-675-908A-8 \$ US-09-967-908A-6 \$ US-09-967-908A-6 \$ US-09-967-908A-6 \$ US-09-967-908A-6 \$ US-09-521-780-5 \$ Sequence 4, Appl 9 US-09-521-780-5 \$ Sequence 5, Appl 1 US-08-126-833-2 \$ Sequence 6, Appl 9 US-09-521-780-5 \$ Sequence 6, Appl 1 US-08-126-833-2 \$ Sequence 6, Appl 9 US-09-521-780-6 \$ Sequence 6, Appl 9 US-09-521-780-6 \$ Sequence 6, Appl 9 US-09-328-352-4627 \$ Sequence 2, Appl 9 US-09-28-352-4627 \$ Sequence 2, Appl 9 US-08-28-1180-2
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stent No. 520615 Sequence 20, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 4, Appl Sequence 5, Appl Sequence 6, Appl Sequence 6, Appl Sequence 7, Appl Sequence 7, Appl Sequence 8, Appl Sequence 6, Appl
520615 , Appl 4, App 4, Appl 4, Appl 4, Appl 5, Appl 7, Appl 7

ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: Muir, Tom
APPLICANT: Mayville, Pattricia
APPLICANT: Mayville, Pattricia
APPLICANT: Mo. 6337385ick, Richard P.
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NUMBER: US/09/339,511
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 9
TYPE: PAT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
NAME/KEY: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position.
US-09-339-511-7
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Muir, Tom
Mayville, Patrici
No. 6337385ick, F
Beavis, Ronald
Ji, Guangyong
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                                                                              GENERAL INFORMATION:
APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN
FILE REFERENCE: 63753/7
CURRENT APPLICATION UNMBER: US/08/861,476C
CURRENT FILING DATE: 1997-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 63753/7
CURRENT APPLICATION NUMBER: US/08/861,476C
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 7; Conserv
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APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
                                                                                                                                                                                              Sequence 6, Application US/08861476C
Patent No. 6447786
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                                              SOFTWARE: PatentIn SEQ ID NO 6
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CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 199-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 9
TYPE: PRT
ORGANISM: Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino
ORGANISM: Staphylococcus aureus
                               ENGTH: 47
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IBR INFORMATION: peptide
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8; Conser
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                                                                 version 3.0
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Pred. No.
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Best Local S
Matches 6
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                                                                                                            Patent No.
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                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (6.19) 535-8949
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, VeCURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,807A
FILING DATE: 08-JUN-193
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
                           ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Diego
STATE: California
COUNTRY: United States
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                  ECOMMUNICATION INFORMATION: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,
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SER OF SEQUENCES:
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                                                                                                              18, Application US/08073807A
5. 5646248
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                                                                                                INFORMATION:
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4370 La Jolla Village Drive, Suite 700
                                                  Sawada, Ritsuko
Lowe, John B.
Fukuda, Minoru
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          CELL SURFACE LAMP EXPRESSION AND SELECTIN-DEPENDENT ADHESION 18
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Pred. No. 49;
1; Mismatches
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Pred. No. 2
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US-08-073-807A-2
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Best Local Similarity 66.7%;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,807A
FILING DATE: 08-JUN-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ent No.
                                                                                                      FILING DATE: 08-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER OF SEQUENCES:
                                               NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9567
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4370 La Jolla Village
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                 (619)
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535-8949
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SELECTIN-DEPENDENT
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Pred. No. 53;
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                                                                                                                                                                                                                                                                   US-09-832-498-2
, LENGTH: 614
, TYPE: PRT
, ORGANISM: Geniculosporium sp.
; 05-832-498-2
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Best Local Similarity 66.
"Arches 6; Conservative
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                   SEQ ID NO 2
                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                Sequence 2, Application US/09832498 Patent No. 6410291
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                               FILE REFERENCE: 10040.200-US
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2001-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Expression Vectors for Stimulating an TITLE OF INVENTION: Immune Response and Methods of Using the Same FILE REFERENCE: 39963-20022.01
                                                                                 NUMBER OF SEQ ID NO
SOFTWARE: PatentIn
                                                                                                                                                APPLICANT: Schneider, Palle
TITLE OF INVENTION: Polypeptides having haloperoxidase activity
FILE REFERENCE: 10040.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/311,784A
CURRENT FILING DATE: 1999-05-13
                                                                                                                                                                                  APPLICANT: Danielsen, Steffen
APPLICANT: Schneider, Palle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Epimmune Inc.
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                                                                                 version 3.0
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                                                                                                                  2001-04-11
                                                                                                                                    US/09/832,498
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Pred. No.
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Pred. No. 59;
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59;
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; OTHER INFORMATION: Xaa represents any US-09-339-511-5
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US-09-832-614A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Pate
SEQ ID NO 2
LENGTH: 614
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Best Local S
Matches
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Patent No. 6337385
GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: No. 64102920zymes A/S
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        Query Match
Best Local Similarity
Matches 7; Conserv
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SEQ ID NO 5
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CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-339-511-5
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                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                          PRICANT: Ji, Guangyong
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Mayville, Patricia
No. 6337385ick, Richard
Beavis, Ronald
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Schneider, Palle
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                        74.48;
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66.7%;
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Pred. No.
            1; Mismatches
                          Score 29; DB 4;
Pred. No. 2.5e+05;
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            1; Indels
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                                          Length 9;
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Best Local S
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APPLICANT: Dumas Milne Edwards, Jean-Baptiste
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APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1990-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
                                                                                                                                                                                            FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
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SOFTWARE: PatentIn V
                   PRIOR FILING DATE: 1996-09-04
PRIOR FILING DATE: 1998-09-04
                                                                                                            PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 9
                                                               PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-08-10
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                                                                                                                                                                                                                                                                                                               PLICANT: Bougueleret, Lydie
TLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
                                                                                                 FILING DATE: 1998-04-13
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SEQ ID NOS:
Patent.pm
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Mayville, Patric
No. 6337385ick,
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -45..-1
US-09-663-600A-197
RESULT 15
US-09-339-511-2
US-09-339-511-2
; Sequence 2, Application US/09339511
; Patent No. 6337385
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
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; Sequence 197, Application US/09663600A
; Patent No. 6573068
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LENGTH: 273
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SOFTWARE: Patent.pm
SEQ ID NO 197
LENGTH: 273
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Best Local Similarity 66.7%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dumas Milne Edwards, Jean-Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: SIGNAL
LOCATION: -45..-1
NAME/KEY: UNSURE
LOCATION: 181,187,193,196,198,199,203,212,214
OTHER INFORMATION: Xaa = any one of the twenty amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1998-08-10
APPLICATION NUMBER: 60/099,273
FILING DATE: 1998-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/096,116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1998-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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Bougueleret, Lydie
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Pred. No. 61;
1; Mismatches

    Mismatches

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Pred. No. 61;
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APPLICANT: J1, Guangyong
ITITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
ITITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-221N
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
CREANISM: Artificial Sequence
FEATURE:
FEATURE:
                                                                                                                                                                                                                                                       ; NAME/KEY: VARIANT; LOCATION: (5); LOCATION: (5); OTHER INFORMATION: Xaa represents any amino acid at this position. US-09-339-511-2
Search completed: January 29, 2004, 15:03:22 Job time: 11.1176 secs
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Best Local
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                                                                                      1 GANAXSSLF
                                                                                                                          1 GVNAXSSAF
                                                                                                                                                                       Similarity 7; Conserv
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No. 6337385ick, Richard
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                                                                                                                                                                          Conservative
                                                                                                                                                                                          71.8%; Score 28; DB 4; Length 9; 77.8%; Pred. No. 2.5e+05;
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maximum Match 100%
Listing first 45 summaries
                                                777766.99.5.1
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                   / Ggn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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2-6/ptodata/1/pubbaa/US06_NEW_PUB.pep.*
2-6/ptodata/1/pubbaa/US06_NEW_PUB.pep.*
2-6/ptodata/1/pubbaa/US07_NEW_PUB.pep.*
2-6/ptodata/1/pubbaa/US08_PUBCOMB.pep.*
2-6/ptodata/1/pubbaa/US08_PUBCOMB.pep.*
2-6/ptodata/1/pubbaa/US08_PUBCOMB.pep.*
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147
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                                                    US-10-032-950-7
US-10-032-950-1
US-10-201-444-6
US-10-201-444-6
US-10-080-170-158
US-10-080-170-538
US-10-371-645-26
US-10-371-645-26
US-10-371-645-26
US-10-371-645-26
US-10-371-63-26
US-10-312-950-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Search time 25.5441 Seconds (without alignments) 73.223 Million cell updates/sec
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                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                        Sequence 7, Sequence 1, Sequence 3,
Sequence
Sequence
Sequence
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Sequence
Sequence
Sequence
Sequence
Sequence
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Sequence
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1, Appli
3, Appli
155, Appl
155, App
538, Appl
538, Appl
26, Appl
26, Appl
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Appl
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US-10-032-950-7
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                                                                         Matches
                                                                                      Query Match
Best Local 9
     GVNAXSSAF 9
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269	247	246	246	243	243	237	237	237	237	144	67	<u>ა</u>	866	583	533	451	416	416	416	405	109	80	9	σħ.	3635	287	273	273	273
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0-369-493-72	-10-369-493-1	-10-125-540-303	09-764-870-30	-10-125-540-4	09-764-870-46	-10-264-237-26	-09-751-708A-49	-09-870-759-49	-09-862-802	08A-60	-10-156-761-825	-09-864-408A	-10-116-275-18	09-810-264-38	-10-373-238-17	-10-156-761-	-09-742-581-2	-09-742-580-	09-742-582-2	-10-156-761-1	-09-975-719-89	09-864-761-43	-10-032-950-2	-10-037-182-	-09-845-58	-10-106-698-477	-10-295-027-12	-10-295-027-	9-981-15 1A -6
equence 72	equence 19925,	e 303	quence 303,	equence 46	ce 464,	equence 2	equence 4	equence 4	equence 2	Sequence 600, App	equence 8	equence 1	equence 1	quence 38	equence 1	1	equence 2	equence 2	quence 2,	equence 1	ce 8	quence 43	2, App	equence 4, App	equence 2, App	equence 4775,	quence 1250,	equence 344, A	ហ

ALIGNMENTS

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US-10-032-950-7
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TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT ETLING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR RILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
SECOND. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Muir. Tom
APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453Alick, Richard
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                          OTHER INFORMATION: Xaa represents any amino
1 GVNAXSSAF 9
                                                     Similarity
9; Conserv
                                                       Conservative
                                                                         94.9%; Score 37;
100.0%; Pred. No.
                                                       0
                                                          Mismatches
                                                                            DB 13; Length 9; 7e+05;
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US-10-032-950-1

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                                                                                                                                                ; ORGANISM: Staphylococcus aureus 
US-10-201-444-3
                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE: 63753/7
CURRENT APPLICATION NUMBER: US/10/201,444
CURRENT FILING DATE: 2002-07-23
FRIOR APPLICATION NUMBER: US/08/861,476
PRIOR PILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 9
TUDE: Nom
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Publication No. US20030078378A1
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Best Local
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Best Local
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                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPPYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
TITLE OF INVENTION: INTERFERENCE
CURRENT FAPPLICATION NUMBER: US/10/032,950
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILLING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEO ID NOS: 8
SOFTMARE: Patentin Ver. 2.0
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OTHER INFORMATION: I
NAME/KEY: VARIANT
LOCATION: (5)
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APPLICANT: Mayville,
APPLICANT: No. US200
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa represents any amino acid at this position
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                                  1 GVNAXSSAF 9
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8; Conservative
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No. US20020077453Alick, Richard
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                                                                        Conservative
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                                                                                        79.5%;
77.8%;
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Pred. No. 7e+0
0; Mismatches
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                                                                                        Score 31; DB 15;
Pred. No. 7e+05;
                                                                        Mismatches
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7e+05;
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RESULT 4 US-10-201-444-6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Mycobacterium leprae US-10-080-170-155
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APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE: 63753/7
CURRENT FILING DATE: US/02/201,444
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US/08/861,476
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 155, Applic
Publication No. US20
GENERAL INFORMATION:
APPLICANT: COLE, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 155
LENGTH: 163
                                                                                                                                                                                                         Sequence 538, Applic Publication No. US20 GENERAL INFORMATION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
GURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION UNUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAY TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES FILE REFERENCE: 03495,0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR PELICATION NUMBER: 60/270,123
PRIOR PELICATION NUMBER: 60/270,123
PRIOR PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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les 7; Conserv
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Similarity 77.8%;
7; Conservation
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Pred. No. 6.8;
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Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                 US-10-371-645-26
                                                                                                                                                                                                                                                                  RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-371-069-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/078,904
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 416
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
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SEQ ID NO 538
LENGTH: 167
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                                                                                                                                                                                                              Sequence 26, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local
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APPLICANT: Epinmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
TITLE OF INVENTION: Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-20022.10
CURRENT APPLICATION NUMBER: US/10/371,069
CURRENT FILING DATE: 2003-02-21
                                                                                                                             APPLICANT:
                                                                                                                                                            APPLICANT: EPIMMUNE Inc. APPLICANT: Fikes, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: human lysosomal membrane glycoprotein-1 (LAMP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ICANT: Livingston, Brian
ICANT: Chesnut, Robert W.
ICANT: Epimmune Inc.
OF INVENTION: Expression Vectors for Stimulating an
OF INVENTION: Immune Response and Methods of Using the Same
REFERENCE: 39963-20022.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION
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                                                                                                                                                                                                                                                                                                                         GMNASSSRF 298
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                                                                                                                         Fikes, John D.
Hermanson, Gary G.
Sette, Alessandro
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Ishioka, Glenn Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hermanson, Gary G
                                                                                                                                                                                                              Application US/10371645
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                                                                                                            Ishioka, Glenn Y.
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66.7%;
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Pred. No. 47;
0; Mismatches
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Pred. No. 1.3e+02;
1; Mismatches 2
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APPLICANT: ISHICKS, Glenn Y.
APPLICANT: Livingscon, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Chesnut, Robert W.
APPLICANT: Epinmune Inc.
ITILE OF INVENTION: Expression Vectors for Stimulating an ITILE OF INVENTION: Expression Vectors for Stimulating an CURRENT APPLICATION NUMBER: US/10/371,260
CURRENT APPLICATION NUMBER: US/09/078,904
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NO 26
SEQ ID NO 26
LENGTH: 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/371,645
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/078,904
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-15
PRIOR REPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FRETENSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 416
TYPE: PRI
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                                                                                                                                                    , OTHER INFORMATION: human lysosomal membrane glycoprotein-1 (LAMP-1) US-10-371-260-26
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                                                                                            Query Match
Best Local (
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                                                                       Matches
                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: human lysosomal membrane glycoprotein-1 (LAMP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
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nes 6; Conserv
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290 GMNASSSRF 298
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                                                                       Similarity 66. 6; Conservative
                                   GVNAXSSAF 9
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66.7%;
                                                                                            76.9%;
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Pred. No. 1.3e+02;
                                                                                            Score 30;
Pred. No.
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Sequence 2, Application US/10151557

Publication No. US20020183506A1

GENERAL INFORMATION:
APPLICANT: No. US20020183506A10zymes A/S

APPLICANT: Danielsen, Steffen

RESULT 10 US-10-151-557-2

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Query Match
Best Local Similarity
Tarches 7; Conserve
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JS-10-151-557-2
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Best Local (
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SEQ ID NO 2
                                                            GENERAL INFORMATION
                                                                          Sequence 6, Application US/10032950 Publication No. US20020077453A1
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CURRENT FILING DATE: 2002-05-18
PRIOR APPLICATION NUMBER: US/09/832,614A
PRIOR FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 600-1-231N
CUTRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453Alick, Richard F.
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TITLE OF INVENTION: Nucleic acids encoding polypeptides having
TITLE OF INVENTION: haloperoxidase activity
FILE REFERENCE: 10173.200_US
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IITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
IITLE OF INVENTION: INTERFERENCE
                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position
                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 614
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No. US20020077453Alick, Richard
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                                                                                                                                                                                                                                                                                           74.48;
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Pred. No.
                                                                                                                                                                                                                                                                                           Score 29; DB 13; Length 9; Pred. No. 7e+05;
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; LOCATION: 181,187,193,196,198,199,203,212,214; OTHER INFORMATION: Xaa = any one of the twenty amino acids US-10-319-763-103
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APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
                                                                                                                                                                                                                                                                          SOFTWARE: Patent.pm
SEQ ID NO 103
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Publication No.
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Best Local
  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILLING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILLING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILLING DATE: 1998-02-09
PRIOR FILLING DATE: 1998-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/319,763
CURRENT FILING DATE: 2002-12-10
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 229
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CONAS FOR SECRETED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa represents any amino acid
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                                                                                                                                                                          NAME/KEY: SIGNAL
                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                        FEATURE
                                                                                                                                                         LOCATION: -45..-1
                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/081,563
FILING DATE: 1998-04-13
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/096,116
                                                                                                                                                                                                                                                                                                                                                                             LING DATE: 1998-08-
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7; Conserv
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o. US20030144490A1
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  74.48;
Score 29; DB 12;
Pred. No. 1.4e+02;
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Pred. No. 7e+05;
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                  Length 273;
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -45..-1
US-10-319-763-197
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US-10-319-763-197
; Sequence 197, A
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CURRENT APPLICATION NUMBER: US/10/319,763
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/066.677
PRIOR FILING DATE: 1997-11-13
PRIOR PELING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR PELING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR PELICATION NUMBER: 60/081,563
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR APPLICATION NUMBER: 60/099,273
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SEQ ID NO 197
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                      -09-981-151A-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dumas Milne Edwards, Jean-Baptiste
                                                                                                                                                                                                                                                                                                                           APPLICANT: Edinger, Shlomit R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: Duclert, Aymeric
PPLICANT: Bougueleret, Lydie
ITLE OF INVENTION: EXTENDED CONAS FOR SECRETED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
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Malyankar, Muriel M
Smithson, Glennda
                                                                                                                                                                                                                                                                                                                                                                    Application US/09981151A
                                                                                                                                                                                   Millet, Isabelle
Peyman, John A
Stone, David J
                                                                             Ellerman, Karen
Shimkets, Richard A
Padigaru, Muralidhara
Guo, Xiaojia
Patturajan, Meera
Taupier Jr, Raymond J
Burgess, Catherine E
Zerhusen, Bryan D
                                                                                                                                                               Gunther, Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/10319763
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                                                                                                                                                                                                                                                                                                         Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.4%; Score 29; DB 12; Length 273; 66.7%; Pred. No. 1.4e+02; Live 1; Mismatches 2; Indels
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Search completed: January 29, 2004, 15:01:46
Job time: 25.5441 secs

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APPLICANT: Gorman, Linda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-168
CURRENT APPLICATION NUMBER: US/09/981,151A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/241,040
PRIOR TILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/241,058
PRIOR APPLICATION NUMBER: 60/241,063
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/241,243
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/241,243
PRIOR APPLICATION NUMBER: 60/241,243
PRIOR APPLICATION NUMBER: 60/241,243
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/242,482
PRIOR APPLICATION NUMBER: 60/242,482
PRIOR APPLICATION NUMBER: 60/242,482
PRIOR APPLICATION NUMBER: 60/242,482
                                              á
                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-151A-64
                                                                                                                                                                                                                                                                SEQ ID NO 64
LENGTH: 273
                                                                                                  Matches
                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                 Remaining Prior Application NUMBER OF SEQ ID NOS: 160 SOFTWARE: PatentIn Ver. 2
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/242,612
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,880
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,881
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
                                                                                                                       Local
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12 GVNKYSTAF 20
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                                                                                             74.4%;
nilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                  Application data removed - See File Wrapper or PALM.
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AAW10778 AAW10779 AAW10784

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Title:
Perfect score:
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2: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

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9: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

10: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

11: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

12: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

13: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

14: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

15: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

16: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

17: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

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20: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

21: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

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length: 2000000000
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Gapop 10.0 , Gapext
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Maximum Match 100%
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AAY67858
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AAM50906
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Compugen Ltd
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Antibacterial cycl
S. aureus peptide
Cyclic peptide SEQ
AgrD-autoinducing
Fusinus inhibitory
Ferritin motif #26
Synthetic ferritin
Synthetic ferritin
Synthetic ferritin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell wall protein production; prophylaxis; exotoxin secretion; bacterial infection; toxic shock syndrome; Staphylococci; Staphylococcus aureus; coagulase-negative S, epidermidis; medical implant infection; cyclic.
                                                                                                                                                                                                                         Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                          Cyclic peptide; modulator; agr response; virulence;
     26-NOV-1997;
                                       24-NOV-1998;
                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial cyclic oligopeptide for Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1999
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                                                                            03-JUN-1999
                                                                                                               WO9926968-A1
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     97GB-0024859
                                         98WO-GB03497
                                                                                                                                               Location/Qualifiers

1..4
/note= "linked by -O-CH(NHX)-(CH2)n-S, where comprises 2-5 amino acids, and is not Gly-Val-Asn-Ala (Claim 1) or is Gly-Val-Asn-Ala (Claim 8)"
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AAM51005 ABB07159 AAM51004

ALIGNMENTS

AAW10801
AAW10802
ABG96785
AAW25556
AAW69684
AAW8323
AAX67867851
AAX767852
AAX767861
AAX767861
AAX6786821

Ferritin motif #21
Ferritin motif #22
Ferritin motif #44
Ferritin motif #47
Ferritin moti

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RESULT 2
AAY67858
ID AAY6
XX AAC AAY6
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CX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Affas ZM,
Williams I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus infection; cyclic peptide; AgrD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S. aureus peptide #8 used for bacterial interference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page -; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyclic antibacterial peptides
       WPI;
                                                                                               (UYRQ )
                                                                                                                                                                                                              24-JUN-1999;
                                                                                                                                                                                                                                                                                                                WO9967286-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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                                                  Muir TW,
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                                               Mayville P,
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                                                                                               ROCKEFELLER.
NEW YORK STATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.7%; Sur.
100.0%; Pr
                                                  Novick
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                                                                                                                                                                                                                                                                                                                                                           "N-terminal residue is linked to the residue to form a cyclic peptide"
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0; Mismatches
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ABP53540 to ABP53547 represent cyclic peptides (I) from the present invention. The present invention also describes a method for treati Staphylococcus aureus infection comprising the administration of a
                                                                    New
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The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of Staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is a secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. Preferred peptides may have the sequence NH2-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z residue and COOH other than a thioester bond, where X is an amino acid, an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The cyclic bond is especially a lactam or lactone bond. The thiololactone
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inhibitor. The peptides are useful
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                                                                                    The peptide was isolated from Fusinus perplex ferruginaus neuroganglia and inhibits muscular contraction, especially of the radular tractile muscle in F.perplex ferrugineus, Prosobranchia and other Mollusca. Alternatively, it can be synthesised by solidand other Mollusca. One or both of the Ser residues at positions 1 or phase techniques. One or both of the Ser residues at positions 1 or 2 may be absent. The peptide can be used in biological studies for the development of drugs. See also AAR10516-R10518 and AAR10520.
                                                                                                                                                                                                                                         Muscular contraction-inhibitory neuro-peptide(s) in mollusca
prepd. by purifying oligopeptide using high power liq.
chromatography after extracting neuro-ganglion of Fusinus per
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    DB 12; I
9.3e+05;
thes 0;
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AAW10783 standard; peptide; 6 AA

25-MAR-2003 10-NOV-1997 (updated)
(first entry)

Ferritin motif #26 important for selective binding affinity

Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; ferritin; myosin light chain; troponin; follicle stimulating hormone; human; growth hormone; immunoglobulin E; prolactin; parathyroid hormone; placental lactogen; hepatitis antigen; antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus; Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.

Synthetic

19-DEC-1996

07-JUN-1996; 96WO-US10498

07-JUN-1995; 95US-0476375

(CYTO-) CYTOGEN CORP

F۷,

Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules such as ferritin

51; Page 56; 156pp; English

This sequence represents a peptide motif derived from ferritin which is comportant for selective binding affinity. Peptides containing motifs such as this may be used as functional surrogates in the conjugate of the invention. The novel labelled conjugate comprises at least one conjugate is capable of competing effectively with the analyte of the surrogate is capable of competing effectively with the analyte of the affinity receptor and this activity can be measured and related to the amount of the analyte present in a sample. Functional surrogate is capable of compete effectively and with the analyte for a limiting amount of the analyte present in a sample. Functional surrogates such as this have an immunoreactive group that allows the surrogate to compete effectively and with the analyte for a limiting amount of its affinity receptor. Functional surrogates are able to mimic naturally cocurring analytes. They can be labelled for use in standard competitive markers, elegen, homogenous immunoassays) for detecting large marromolecules such as polypeptides, polysaccharides, polynuclectides, glycoproteins and lipid-containing macromolecules, as well as small captogens. Typical diagnostic analytes for detection include cardiac or tumour markers, allergens, hormones related to fertility-pregnancy or analytes associated with infectious disease. In particular, the assays are useful for detecting ferritin, follicle stimulating hormone, human considered to consider a sample assays are useful actogen, hepatitis antigens or antibodies against them, human considered to consider a sample and them are provided hormone, human procental lactogen, hepatitis antigens or antibodies against them, human considered to consider a sample and the sample and to consider a sample and the
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9.3e+05;
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9508-0476375

(CYTO-) CYTOGEN CORP

Lee-owen F۷ Carter

Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules such as ferritin $% \left(1\right) =\left\{ 1\right\} =\left$

Claim 51; 26; 156pp; English

This sequence represents a synthetic ferritin peptide which was used as functional surrogate in the conjugate of the invention. The novel capabiled conjugate comparises at least one label attached to a functional surrogate of an analyte of interest. The surrogate is capable of competing effectively with the analyte for a limiting amount of an capabile of capabile of capabile for the analyte of that is altered upon interaction with the affinity receptor and this capabile. Functional surrogates such as this have an immunoreactive group that allows the surrogates such as this have an immunoreactive canalyte for a limiting amount of its affinity receptor. Punctional surrogates are able to mimic naturally occurring analytes. They can be labelled for use in standard compete effectively and with the canalyte for a bit to mimic naturally occurring analytes. They can be labelled for use in standard compete effectively assays (esp. copypeptides, polymorphic surface), polymorphic surfaces such as glycoproteins and copypeptides, polymorphic such as glycoproteins and copypeptides, polymorphic such as surfaces and control of the same and copypeptides, polymorphic such as glycoproteins and control of the same and copypeptides. polypeptides, polysaccharides, lipid-containing macromolecule macromolecules, as well as small

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Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic analytes for detection include cardiac or tumour markers, allergens, hormones related to fertility-pregnancy or analytes associated with infectious disease. In particular, the assays are useful for detecting ferritin, follicle stimulating hormone, human growth hormone, immunoglobulin E, prolactin, parathyroid hormone, human placental lactogen, hepatitis antigens or antibodies against them, human chorionic gonadotropin, human luteinising hormone, cytomegalovirus, Chlamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin, carcincembryonic antigen, alpha-fetoprotein, prosteate-specific antigen and CA125 (a tumour marker). (Updated on 25-MAR-2003 to correct PI field.)
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This sequence represents a synthetic ferritin peptide which was used as a functional surrogate in the conjugate of the invention. The novel labelled conjugate comprises at least one label attached to a functional
                                                             Claim 51;
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                                                           26; 156pp; English.
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100.0%; Pred. No. 9.3
tive 0; Mismatches
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esp. for detecting
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9.3e+05;
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ng large macromolecules
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(first entry)
                                                                                                  Carter JM;
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. 9.3e+05;
ches 0;
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10-NOV-1997
                                                                                                                                                                                                    Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunosassay; detection; diagnostic analyte; Chlamydia; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; ferritin; myosin light chain; troponin; follicle stimulating hormone; human; growth hormone; immunoglobulin E; prolactin; parathyroid hormone; placental lactogen; hepatitis antigen; antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus; streptcococus; rubella; toxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
                      07-JUN-1996;
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Pred. No.
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This sequence represents a peptide motif derived from ferritin which is comportant for selective binding affinity. Peptides containing motifs consumed that the conjugate of the invention. The novel labelled conjugate comprises at least one comparises at least one comparises at least one conjugate exhibits an activity that is altered upon interaction with the analyte conjugate exhibits an activity that is altered upon interaction with conjugate exhibits an activity that is altered upon interaction with comparise this have an immunoreactive group that allows the surrogates such as this have an immunoreactive group that allows the surrogate to compete effectively and with the analyte for a limiting amount of its compete effectively and with the analyte for use in standard competitive affinity receptor. Functional surrogates are able to mimic naturally occurring analytes. They can be labelled for use in standard competitive affinity assays (esp. homogenous immunoassays) for detecting large containing macromolecules, as well as small containing macromolecules, as well as small containing macromolecules as well as small containing macromolecules. Typical diagnostic analytes for detection include cardiac or tumour markers, allergens, hormones related to fertility-pregnancy or canalytes associated with infectious disease. In particular, the assays are useful for detecting ferritin, follicle stimulating hormone, human containing containing hormone, human containing containing hormone, which human containing hormone, cytomegalovirus, of containing hormone, cytomegalovirus, containing hormone, cytomegalovirus, cont
                                                      myoglobin, myosin light chain, troponin, carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen and CA125 (a tumour m (Updated on 25-MAR-2003 to correct PI field.)
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Sequence AA;

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Query Match
Best Local S
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SSLF 5
                  Conservative
             94.7%; but
100.0%; Pr
                        Score 18;
Pred. No.
                 DB 18; I
, 9.3e+05;
thes 0;
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RESULT 11
AAW10779
ID AAW10
XX AAW10
AC AAW10
XX 25-MA10
XX 25-MA10
XX POINT
XX FUNCT
XX FUNCT
XX FUNCT
XXW FUNCT
XXW POINT
XXW Cardy
XXW pregyl
XXW prolk
XXW prolk
XXW prolk
XXW AMTIN 25-MAR-2003 10-NOV-1997 AAW10779 standard; peptide; 7 AA AAW10779;

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Ferritin motif #22 important for selective binding affinity.

(updated) (first entry)

Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; ferritin; myosin light chain; troponin; pregnancy; infectious disease; ferritin; myosin light chain; troponin; follicle stimulating hormone; human; growth hormone; immunoglobulin E; prolactin; parathyroid hormone; placental lactogen; hepatitis antigen; antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus

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AAW10784
ID AAW
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DT 25-I
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                                                                                                                                                                                                                                                                                                                                                                       CC conjugate exhibits an activity that is altered upon interaction with CC the affinity receptor and this activity can be measured and related to CC the amount of the analyte present in a sample. Functional surrogates CC such as this have an immunoreactive group that allows the surrogate to CC compete effectively and with the analyte for a limiting amount of its CC affinity receptor. Functional surrogates are able to mimic naturally CC occurring analytes. They can be labelled for use in standard competitive CC affinity assays (esp. homogenous immunoassays) for detecting large CC macromolecules such as polypeptides, polypaccharides, polypucleotides, CC glycoproteins and lipid-containing macromolecules, as well as small CC tumour markers, allergens, hormones related to fertility-pregnancy or CC analytes associated with infectious disease. In particular, the assays CC are useful for detecting ferritin, follicle stimulating hormone, human CC placental lactogen, hepatitis antigens or antibodies against them, human CC chamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, CC myoglobin, myosin light chain, troponin, carcinoembryonic anatigen, CC climare for teaching the prostate-specific antigen and CA125 (a tumour marker). CC (Updated on 25-MAR-2003 to correct PI field.)
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Best Local S
Matches 4
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  25-MAR-2003
10-NOV-1997
                                                          AAW10784;
                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                            peptide;
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Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; ferritin; myosin light chain; troponin; follicle stimulating hormone; human; growth hormone; immunoglobulin E; prolactin; parathyroid hormone; placental lacrogen; hepatitis antigen; antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus; streptcocccus; rubella; tcxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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WO9641172-A1

19-DEC-1996

07-JUN-1996; 96WO-US10498

07-JUN-1995; 95US-0476375

(CYTO-) CYTOGEN CORP

Lee-owen FV, Carter JM

WPI; 1997-077284/07

Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules such as ferritin $\,$

Claim 51; Page 56; 156pp; English

CC such as this may be used as functional surrogates in the conjugate of the invention. The novel labelled conjugate comprises at least one Clabel attached to a functional surrogate of an analyte of interest. CC The surrogate is capable of competing effectively with the analyte CC for a limiting amount of an affinity receptor for the analyte. The CC conjugate exhibits an activity that is altered upon interaction with CC the affinity receptor and this activity can be measured and related to CC the amount of the analyte present in a sample. Functional surrogate s such as this have an immunoreactive group that allows the surrogates cc such as this have an immunoreactive group that allows the surrogate occurring analytes. They can be labelled for use in standard competitive concurring analytes. They can be labelled for use in standard competitive concurring analytes such as polypeptides, polysaccharides, polynucleotides, glycoproteins and lipid-containing macromolecules, as well as small cc macromolecules as well as small cc manufactory or can analytes associated with infectious disease. In particular, the assays care useful for detecting ferritin, follicle stimulating hormone, human cc placental lactogen, hepatitis antigens or antibodies against them, human contains, propaction, parachyroid hormone, human chorionic gonadotropin, human luteinising hormone, cytomegalovirus, composin light chain, tropolasma, herpes virus, DK-MB, cmyclotian, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, contained on 25-MAR-2003 to correct PI field.) This sequence represents a peptide motif derived from ferritin which important for selective binding affinity. Peptides containing motifs such as this may be used as functional surrogates in the conjugate of 18

Sequence ۷, ĀΑ;

δ Query Match Best Local s Matches 4 N 4. Similarity SSLF 5 Conservative 94.7%; Score 18; DB 18; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Length 7; 0 Gaps

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RESULT 13
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macromolecules such as polypeptides, polypeaccharides, polypuclectides, glycoproteins and lipid-containing macromolecules, as well as small haptens. Typical diagnostic analytes for detection include cardiac or tumour markers, allergens, hormones related to fertility-pregnancy or analytes associated with infectious disease. In particular, the assays are useful for detecting ferritin, follicle stimulating hormone, human growth hormone, immunoglobulin E, prolactin, parathyroid hormone, human placental lactogen, hepatitis antigens or antibodies against them, human chorionic gonadotropin, human lutteinising hormone, cytomegalovirus, chlamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin, carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen and CA125 (a tumour marker). (Updated on 25-MAR-2003 to correct PI field.)
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10-NOV-1997
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RESULT 14
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This sequence represents a peptide motif derived from ferritin which is comportant for selective binding affinity. Peptides containing motifs consuch as this may be used as functional surrogates in the conjugate of the invention. The novel labelled conjugate composises at least one compared to a functional surrogate of an analyte of interest. The surrogate is capable of competing effectively with the analyte conjugate exhibits an activity that is altered upon interaction with conjugate exhibits an activity that is altered upon interaction with conjugate exhibits an activity that is altered upon interaction with conjugate exhibits an activity that is altered upon interaction with confidence in the analyte present in a sample. Punctional surrogates compete effectively and with the analyte for a limiting amount of its compete effectively and with the analyte for a limiting amount of its compete effectively and with the analyte for a limiting amount of its compete effectively and with the analyte for a limiting amount of its compete effectively analytes. They can be labelled for use in standard competitive affinity assays (esp. homogenous immunoassays) for detecting large macromolecules and lipid-containing macromolecules, as well as small containing macromolecules, as well as small containing macromolecules, as well as small contains.
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Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                      Claim 56; Page 56; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125
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10-NOV-1997
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100.0%; Pr
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Pred. No. 9.3
0; Mismatches
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RESULT 15
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Matches
The invention describes a method of producing soluble human leukocyte antigen (HLA) molecules (SHLA) in cell pharm involving amplifying HLA allelic DNA by PCR using a locus specific primer to produce truncated a PCR product (PI), inserting P1 into mammalian expression vector; electroporating the plasmid into a host cell; inoculating the cell pharm with the host cell such that cell pharm produces SHLA. A multimeric HLA complex (I) is useful for testing functionality of peptide ligands bound by at least two soluble HLA molecules. (I) can be tested for its ability to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour markers, allergens, hormones related to fertility-pregnancy or analytes associated with infectious disease. In particular, the assays are useful for detecting ferritin, follicle stimulating hormone, human growth hormone, immunoglobulin E, prolactin, parathyroid hormone, human placental lactogen, hepatitis antigens or antibodies against them, human chorionic gonadotropin, human lutteinising hormone, cytomegalovirus, Chlamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin, carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen and CA125 (a tumour marker) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soluble human leukocyte antigen; HLA; sHLA; cell pharm; multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response; viral infection; cancer; autoimmune disease; vaccine development; MHC; major histocompatibility complex; diagnostic development; HLA class I polymorphism; HLA-B15 allotype.
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                                                                                                                                                                                                                                                                                                                                                                                         responses involves using
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(PRIL/)
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18-DEC-2000; 2000US-256410P.
10-OCT-2001; 2001US-0974366.
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                                                                                                                                                                                                                                                                                                                                                                                   soluble human leukocyte antigen (HLA) in cell pharm useful
es of peptide loading for characterizing human immune
involves using HLA allelic cDNA or genomic DNA as starting
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CC responses in humans. (I) is useful for studying T cell responses to pathological conditions such as viral infections and cancer, and for modulating the human immune system to induce tolerance in autoimmune cd. seases. The individual secreted major histocompatibility complex (MHC) molecules produced are useful for studies of peptide loading (i.e., in concine development) and to the development of diagnostics. With the secreted MHC molecules, naturally loaded peptides can be eluted from the CC secreted MHC molecules, naturally loaded peptides can be eluted from the casessment of structural and functional impact of HIA class I sessessment of structural and functional impact of HIA class I collars I HIA-BIS allotypes; compare the different ligand maps to cidentify potentially shared elements; and characterise the elements constitutely potentially shared elements; and characterise the elements constituted to positively or negatively validate the occurrence of commandian or insect/bacterial cells such that milligram or greater quantities of an individual class I or class I molecule can be obtained.

This sequence represents a HIA (human leukocyte antigen) epitope.
Sequence
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Matches Query Match Best Local Similarity 4; Conserv SSLF 5 Conservative 94.7%; 5cc 100.0%; Pr Score 18; DB; pred. No. 9.3 DB 23; I 9.3e+05; Length 7; 0; Gaps

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SSLF 7

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Search completed: January 29, 2004, 14:52:14
Job time: 20.4853 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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1: pir1:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Ig heavy chain V r
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S57518

T cell receptor beta chain V region - human (fragment)

C.Species: Homo sapiens (man)
C.Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C.Pate: 10-Oct-1995 #sequence_revision 17-
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A;Accession: S57518
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-18 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z49920; NID:g887490; PIDN:CAA90166.1; PID:g887491
C;Keywords: T-cell receptor
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Length 18;

45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30
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102	101	101	100	99	97	95	93	93	92	85	84	83	82	80	80
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G71025	T38892	S73700	S44892	F98105	A83971	AG0277	C71984	G64521	QQECXP	C82369	AB2604	C84274	C69013	S19987	S19984
hypothetical prote	very hypothetical	probable lipoprote	ZKll2.4 protein -	conserved hypothet	hypothetical prote	probable phage-rel	hypothetical prote		hypothetical prote	this protein VC006	hypothetical prote				

ALIGNMENTS

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R.Gabrielsson, B.; Fairhall, K.M.; Robinson, I.C.A.F.

J. Endocrinol. 124, 371-380, 1990
A;Title: Growth hormone secretion in the guinea-pig.
A;Reference number: A60739; MUID:90237710; PMID:1970601
A;Accession: A60739
A;Molecule type: protein
A;Residues: 1-20 <GAB>
C;Comment: The growth hormone system in the guinea pig is unusual among mammals in C;Superfamily: prolactin
C;Superfamily: prolactin
                                                                                                                                                                                                                                                                                                                                                 somatotropin - guinea pig (fragment)
N;Alternate names: growth hormone
C;Species: Cavia porcellus (guinea pig)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 17-Mar-1999
C;Accession: A60739
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A60739
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7 SSLF 10
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                                                                            nilarity 100.0%; | Conservative 0;
                                                                          94.7%; Score 18; DB
100.0%; Pred. No. 72,
cive 0; Mismatches
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100.0%; Pred. No. 64;
tive 0; Mismatches
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T-cell receptor alpha chain J region (TA20) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Nov-1999
C;Accession: S03481
R;Arden, B; Klotz, J.L.; Siu, G.; Hood, L.E.
Nature 316, 783-787, 1985
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A; Residues: 1-21 < ARD>
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A;Molecule type: mRNA
A;Residues: 1-10,'A',12-13,'R',15-20,'T',22,'D',24 <MC2>
A;Experimental source: B cell; clone NP-7-12
                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1697, PH1699
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607; PMID:8315385
A;Accession: PH1697
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A; Residues: 1-24 < MCH>
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A; Residues: 1-24 < MCH>
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Ig heavy chain V region - mouse (Ling)
Ig heavy chain V region - mouse mouse)
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;Species: Mus musculus (house mouse)
;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999;Accession: PH1696
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Best Local S
Matches 4
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;Title: Antigen-driven B cell differentiation in vivo.
;Reference number: PH1675; MUID:93301607; PMID:8315385
                                                            Experimental source: B cell; Note: the authors translated Accession: PH1699
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gene
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hypothetical protein ORF34a - Norway spruce chloroplast C;Species: chloroplast Picea abies (Norway spruce) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999 C;Accession: T11814 R;Kluemper, S.; Kanka, S.; Riesner, D.; Etscheid, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: sequence extracted fro C;Superfamily: immunoglobulin C;Keywords: T-cell receptor
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E47719
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                                                                                                                    A;Genome: CHIPPETT
C;Keywords: chloroplast
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A;Title: In vivo clonal dominance and limited T-cell receptor usage
A;Reference number: A47719; MUID:93376774; PMID:8367485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C;Accession: E47719
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A; Accession: T11814
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A;Description: Characterisation of a Norway spruce chloroplast DNA clone: Complete
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A; Residues: 1-29 <WED>
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A;Residues: 1-34 <KLU>
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Pred. No.
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March 1997
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hypothetical protein ECs1538 [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli (C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: B90821

RESULT B90821

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AgrD protein [imported] - Staphylococcus aureus (strain N315)
C.Species: Staphylococcus aureus
C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C.Accession: C89995
R.Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;NEGLUB: F----
A;NOlecule type: DNA
A;Residues: 1-46 <HAY>
A;Residues: 1-46 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34961.1; PID:g13361002; GSPDB:GN00154
A;Cross-references: GB:BA000007; PIDN:BAB34961.1; PID:g13361002; GSPDB:GN00154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. B, 11-22, 2001
A;Tile: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B90821
                                                                                                                     A;Title: The virulence regulator protein of Listeria ivanovii is highly homologous to A;Reference number: 854403; MUID:95075291; PMID:7984088 A;Accession: 854405
                                                                                                                                                                                             C;Species: Listeria ivanovii
C;Datte: 02-Dec-1993 #sequence_revision 25-Oct-1996 #text_change 03-Jun-2002
C;Accession: S54405; S34728
R;Lampidia, R; Gross, R,; Sokolovic, Z.; Goebel, W.; Kreft, J.
                                                                                                                                                                                                                                                                                                              RESULT 10
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               A; Note: the nucleotide
                               A; Experimental source:
                                                A;Cross-references: EMBL:X72685; NID:g396074; PIDN:CAA51232.1; PID:g396077
                                                                  A; Residues: 1
                                                                                   A; Molecule type: DNA
;Genetics:
                                                                                                       Status: nucleic acid sequence not
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4; Conserv
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Yasunaga, T.; Kuhara,
                                                                                                                                                                             13, 141-151, 1994
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               sequence was submitted to the EMBL Data Library, March
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100.0%;
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Shiba, T.;
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Shinagawa, H.
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A;Pathway: nucleotide biosynthesis
C;Superfamily: ribose-phosphate pyrophosphokinase catalytic chain
C;Keywords: diphosphotransferase; magnesium; nucleotide biosynthesis
NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain 5 - C;Species: mitochondrion Artemia sp. (brine shrimp) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text C;Accession: S01877
                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: B71683
R;Andersson, S.G.E.; Zomorodipour, A.; Ande
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia
A;Reference number: A71630; MUID:99039499;
A;Accession: B71683
                                                                        RESULT
S01877
                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-55 < ANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein RP279 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B71683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, June 1996 A;Description: Pea S-adenosylmethionine decarboxylase
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R;Carrasco, P.; Marco,
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C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: T06514
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A; Residues: 1-54 < CAR>
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Pisum sativum (garden
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                                                                                                                                                                                                                            94.7%; Score 18; DB larity 100.0%; Pred. No. 2e Conservative 0; Mismatches
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ce: strain Madrid E
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100.0%; Fi
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tive 0; Mismatches
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                    #text_change 03-Jun-2002
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R.Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor A;Reference number: A72150
A;Accession: H72168
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A;Title: Genome organization of Artemia mitochondrial DNA.
A;Reference number: S01207; MUID:88289417; PMID:3135541
A;Accession: S01877
                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule: 1-62 <SHC>
A;Residues: 1-62 <SHC>
A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54746.1; PID:e1542702; PID:g5830707
A;Experimental source: strain Garcia-1966
A;Experimental source: strain Garcia-1966
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A;Molecule type: DNA
A;Residues: 1-62 «NAK»
A;Cross-references: EMBL:D17510; NID:g529643; PIDN:BAA04348.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein 62b - Japanese black pine chloroplast C;Species: chloroplast Pinus thumbergiana (Japanese black pine) C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 18-Aug-2000 C;Accession: T07470
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                                                                                            A;Gene:
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A;Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome A;Reference number: Z16030; MUID:95024047; PMID:7937893
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A; Residues: 1~59 <BAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                             protein - variola minor virus (strain Garcia-1966)
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  94.7%; Score 18; DB 2; L
ilarity 100.0%; Pred. No. 2.3e+02;
Conservative 0; Mismatches 0;
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100.0%;
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o. 2.3e+02;
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MEDLINE=88289417; PubMed=3135541;
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Eukaryota; Metazoa;
Artemiidae; Artemia.
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MEDLINE=95024047; PubMed=7937893;

MEDLINE=95024047; PubMed=7937893;
                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Stre
Spermatophyta; Coniferopsida;
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                                                                                                                                                                                                                                               Sugiura
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                                                                                                                                                                                                                                                                                                                                                            Pinus thumbergii
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
56-f complex subunit VI (Cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.7%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                           pine)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                            black pine).
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es; Pinaceae; Pinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 59;
                                                                                                                                                                                                                                                                                                                                                                                                b6f complex
                                                                                                                                                                                                                                                          Tsudzuki
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RESULT 4
EX75 CHLPN
ID EX75 C QUELLEN
ID EX75 C QUELLEN
ID 16-CT
DT 16-CT
RA STAIN
RA READ INCLES
RA WHITE
RA GWINN
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Matches
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Q9K1¥4;
16-OCT-2001
                                                                                                                                                                               STRAIN=CWL029;
MEDLINE=99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomat Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Probable exodeoxyribonuclease VII small subunit
(Exonuclease VII small subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D17510; BAA04348.1;
PIR; T07470; T07470.
HAMAP; MF_00433; atypical;
Pfam; PF05115; PetL; 1.
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"Genome sequences of Chlamydia trachomatis MoPn and Chla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=J138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20330349;
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                                                                                                       similarity).
SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95
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Pred. No.
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Chlamydiaceae;
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K., Bass
Dodson R.,
Salzberg
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Q5Z469;
Q5Z469;
30-MAY-2000 (Rel. 39, C
30-MAY-2000 (Rel. 39, D
28-FEB-2003 (Rel. 41, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN PROTEIN EXPORT. PARTICIPATES IN AN EARLY EVENT OF PROTEIN TRANSLOCATION (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: BELONGS TO THE SECG FAMILY.
                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;

Jakoby M.J., Burkovski A., Meier-Wagner J.;

Jakoby M.J., Burkovski A., Meier-Wagner J.;

"Ammonium uptake in Corynebacterium glutamicum is regulated level of expression and enzyme activity.";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001686; -; NOT_ANNOTATED_CDS.
EMBL; AE002238; AAF:8587.1; -.
EMBL; AP002548; -; NOT_ANNOTATED_CDS.
PIR; A81539; A81539.
TIGR; CP0788; -.
                 InterPro, IPR004692; SecG.
Pfam; PF03840; SecG; 1.
PRINTS; PR01651; SECGEXPORT.
TIGRFAMS; TIGR00810; SecG; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       EMBL; AJ007732; CAA07632.1; -. EMBL; AP005279; BAB98977.1; -.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 13032 /
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Translocation;
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RESULT 6
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Kocher T.D., Thomas W.K., Meyer A., Edwards S.V., Paabo S.,

Willablanca F.X., Wilson A.C.;

Willablanca of mitochondrial DNA evolution in animals: amplification

Thomasics of mitochondrial DNA evolution in animals: amplification

and sequencing with conserved primers.";

Proc. Natl. Acad. Sci. U.S.A. 86:6195-6200(1989).

Proc. Natl. Acad. Sci. U.S.A. 86:6195-6200(1989).

Proc. Natl. Acad. Sci. U.S.A. 80:6195-6200(1989).

Proc.
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P16359;
01-AUG-1990
01-AUG-1990
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InterPro; IPR005798; Cytb_b6_C.
InterPro; IPR005797; Cytb_b6_N.
Pfam; PF00033; cytochrome_b_N; 1.
PROSITE; PS00193; CYTCCHROME_B_HEME; 1.
PROSITE; PS00192; CYTCCHROME_B_HEME; 1.
Electron transport; Mitochondrion; Respiratory chain;
                                                                                                                                                                                                                        Heme.
NON TER
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Rodentia; Sciurognathi; Heteromyidae;
Dipodomyinae; Dipodomys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytochrome b (Fragment) MTCYB OR COB OR CYTB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dipodomys californicus (Kangarco rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: The main subunits of complex b-c1 are: cytochrome cytochrome c1 and the Rieske protein (By similarity). SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 SSLF 34
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77 AA;
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37
51
79
9 AA;
94.7%;
(larity 100.0%;
Conservative (
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(Rel. 15, Last sequence update)
(Rel. 42, Last annotation updat
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                                                                                                                             9067 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.7%; but
100.0%; Pr
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75
                                 Score 18;
Pred. No.
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IRON
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POTENTIAL.
                                                                                                                         62F9B7E195C884EE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                79
                                                                                                                                                                                                                                                                                                                       Transmembrane;
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8-13 1-13 1-14 1-17

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RESULT 8
YOG4_CAEEL
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Best Local S
Matches 4
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01-JUL-1993 (
16-OCT-2001 (
Hypothetical
YCF15.
                                                                                                                    P34613;
01-FEB-1994 (
01-FEB-1994 (
28-FEB-2003 (
Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BUNGALYULA; VIRIGIPIANTAE; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II, Myrtales; Onagraceae; Oenothera.
                                                                                                                                                                                                                                                                                                                                                                        PIR; S19984; S19984.
PIR; S19987; S19987.
Chloroplast; Hypothetical p:
SEQUENCE 80 AA; 9408 MW;
SEQUENCE FROM N.A. STRAIN=Bristol N2; MEDLINE=94150718;
                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE=93169690; PubMed=8435856;
Nimzyk R., Shoendorf T., Hachkel W.;
"In-frame length mutations associated with short tandem repeats are
located in unassigned open reading frames of Oenothera chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oenothera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oenothera villaricae,
                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   urr. Genet. 23:265-270(1993).
:- SIMILARITY: BELONGS TO THE YCF15 FAMILY.
                                                                                                                                                                                            CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OENVI
                                                                                                                                                                                                                                                                                                                                                                                                                               X64615; CAA45897.2; -. X64616; CAA45899.2; -.
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                                                                                                                     (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
1 protein ZK112.4 in chromosome III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 26, Created)
(Rel. 26, Last sequence update)
(Rel. 40, Last annotation update)
1 9.4 kDa protein ycf15 (ORF 80).
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                            STANDARD;
  PubMed=7906398;
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                                                                                                                                                                                                                                                                                                                               94.7%;
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                                                                                                                                                                                                                                                                                                                                                                          protein.
4; B5C0BC2D1D354846 CRC64;
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                                                                                                                                                                                                                                                                                                                   Score 18; DB 1; Le
Pred. No. 1.8e+02;
0; Mismatches 0;
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  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                              Length 80
                                                                                  Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
                                                                                                                                                                                                                                                                                                                     0,
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RX MEDILINE-21848401; PubMed=11859360;

RA WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gollins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,

RA Gentles S., Goble A., Hamilin N., Harrits D., Hidalgo J., Hodgson G.,

RA Gentles S., Goble A., Hamilin N., Huckle E.J., Hunt S., Jagels K.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mocney P., Moule S., Mangall K., Murphy L., Niblett D., Odell C.,

RA Mocney P., Moil S., Pearson D., Quall M.A., Rabbinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Rabiron J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S. V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Vanskreels E., Rieger M., Schaefer M., Meller-Auer S.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
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01-0CT-1996 (Rel. 34, C
01-0CT-1996 (Rel. 34, I
28-FEB-2003 (Rel. 41, I
Very hypothetical proti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WormPep; ZK11
Hypothetical
SEQUENCE 10
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulso
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownke
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Watterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHIZOSACCHAROMYCES DOMDE (Fission yeast).

Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetacaaa.

Schizosaccharomycetales; Schizosaccharomycetacaaa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L14324; AAA28187.1; PIR; S44892; S44892.
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STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [_TaxID=4896;
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100 AA; 11248 MW;
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41, Last annotation
protein C4H3.12c in
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100.0%;
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in update)
in chromosome
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P75316;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2011 [ipoprotein MPN467 precursor (P01_orf101).
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GeneDB SPombe; SPAC4H3.12c; -.

Hypothetical protein; Transmembrane.

Hypothetical protein; Transmembrane.

TRANSMEM 25 45 POTENTIAL.

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EMBL; AE000036; AAB96022.1; -. PIR; 873700; S73700.
InterPro; IPR001595; Lipoprotein 3. Pfam; PF00938; Lipoprotein 3; 1. ProDom; PD003276; Lipoprotein 3; 1. PROSITE; PS00013; PROKAR_LIPOPROTEI
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STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMede8948633;
Himmelreich R., Hilbert H., Plagens H.,
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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SIGNAL 1 25 POTENTIAL.
                                 Saccharomyces cerevisiae (Baker's Eukaryota; Fungi; Ascomycota; Sacc Saccharomycetales; Saccharomycetac NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20193820; PubMed=10729156;
Afonso C.L., Tulman E.R., Lu Z., Zsak L.,
"The genome of fowlpox virus.";
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Viruses; dsDNA viruses,
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SEQUENCE FROM N.A.
Pohl T.M., Aljinovic
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P44P_CANMA STANDARD; PRT; 105 AA. (200477; Q00494; 01-NOV-1997 (Rel. 35, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 60S ribosomal protein L44 P (L41) (L41 P-type) L41P1A AND L41P1B.
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Hypothetical protein.
SEQUENCE 104 AA; 123
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                                                                                                                                                                                                                                        Pfam; PF00935; Ribosomal_L44; 1.
ProDom; PD002841; Ribosomal_L44E; 1.
PROSITE; PS01172; RIBOSOMAL_L44E; 1.
                                                                                                                                                                                                                                                                                                                          EMBL; D43686; BAA07782.1; -. EMBL; D43687; BAA07784.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- MISCELLANEOUS: CYCLOHEXIMIDE SENSITIVE TYPE.
-!- SIMILARITY: BELONGS TO THE L44E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eishun M.;
Submitted (DEC-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=IAM 12247;
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                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                  InterPro; IPR000552; Ribosomal L44E
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Score 18; Pred. No.

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Query Match Best Local S Matches

MOD_RES CONFLICT SEQUENCE

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BLOCKED. K -> E (IN REF. 1). K 7B56E7CD5EA89C24 CRC64;

Ribosomal

protein

PIR; S53651; R5UC12. InterPro; IPR001813; 60s_ribosomal. Pfam; PF00428; 60s_ribosomal; 1.

PIR; S53651;

EMBL; X59038; CAA41765.1;

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RESULT 14
RL12_SULAC
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                                                                                                                                                                                                                                                                                                                                          Ramirez C., Shimmin L.C., Newton C.H., Matheson Can. J. Microbiol. 35:975-975 (1989).

-i- FUNCTION: SEEMS TO BE THE BINDING SITE FOR INVOLVED IN PROTEIN SYNTHESIS AND APPEARS 7 ACCUPATE TRANSLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95055761; PubMed=7966335; Ramirez C., Shimmin L.C., Leggatt P., Matheson A.T. "Structure and transcription of the L11-L1-L10-L12 gene operon from the extreme thermophilic archaeon acidocaldarius.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89248688; PubMed=2497941;
Ramirez C., Shimmin L.C., Newton C.H., Matheson A.T.,
"Structure and evolution of the L11, L1, L10, and L12
ribosomal proteins in eubacteria, archaebacteria, and
Can. J. Microbiol. 35:234-244(1989).
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"The complete amino acid sequence of the ribosomal A.
From the archaebacterium Sulfolobus acidocaldarius.";
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STRAIN=ATCC 33909 / NCIB 11770 /
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
CAUTION: WAS ORIGINALLY (REF.3) THOUGHT TO ORIGINATE FROM
S.SOLFATARIOUS STRAIN P1, BUT THE CULTURE WAS CONTAMINATED WITH
                                                                                                                                                                                                                                   S.ACIDOCALDARIUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231:331-335(1988).
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equivalent
leucaryotes.";
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RESULT 15
PT17_STYPL STANDARD; PRT; 112 AA.

ID PT17_STYPL STANDARD; PRT; 112 AA.

AC P28209;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Protein-tyrosine phosphatase 17 (EC 3.1.3.48) (Fragment).

GN STY 17.
Search completed: January 29, 2004, 14:53:12 Job time : 4.23529 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=91139172; PubMed=1704870;
Matthews R.J., Flores E., Thomas M.L.;
"Protein tyrosine phosphatase domains from the protochordate Styela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Styela plicata (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Styelidae; Styela.
NCBI_TaxID=7726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenetics 33:33-41(1991).
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
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Q9R7V1;
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01-MAY-2000
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095795;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
Advanced glycosylation end product-specific receptor
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Blazkova M., Kankova
Submitted (MAY-1998)
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E2 protein (
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NCBI TaxID=11103;
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Bacteria; Firmicutes; Bacillales;
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EMBL; AF473750; AAL86820.1; -.
InterPro; IPR002531; HCV NS1.
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Coat protein; Envelope protein;
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(Genome polyprotein) (Fragment).
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Hepatitis C virus.
Viruses; ssRNA positive-strand
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Viruses; ssRNA pos
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Manzin A., Solforosi L., Debiaggi
Zanetti A.R., Clementi M.;
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Gaudy C., Moreau A.,
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Pfam; PF01560; HCV_NS1; 1.
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Zanetti A.R., Clementi M.;
"Dominant role of host selective pevolution in perinatal infection."
J. Virol. 74:4327-4334 (2000).
EMBL; AF192431; AAF65642.1; -.
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Zanetti A.R., Clementi M.;
Zanetti A.R., Clementi M.;
"Dominant role of host selective pr
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Manzin A., Solfcrosi L., Debiaggi
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"Influence of the dynamics of Hepatitis C virus histological outcome of liver transplantation."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ da EMBL; AF221140; AAF77702.1; -.
InterPro; IPR002531; HCV NS1.
Pfam; PF01560; HCV NS1; I.
Coat protein; Envelope protein; Glycoprotein; No Polyprotein; Transmembrane.
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Gaudy C., Moreau A., Veillon P., Lunel-Fabiani F., Goudeau
"Pretreatment analysis of HCV-1b HVR1 amino acid sequences
differentiate strains resistant and sensitive to antiviral
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF473770; AALB6840.1; -
InterPro; IPR002531; HCV NS1.
Pfam; PF01560; HCV NS1; T.
Coat protein; Envelope protein; Glycoprotein; Nonstructural
             Viruses; ssRNA positive-strand Hepacivirus. NCBI TaxID=11103;
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22, Last annotation update)
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01-JUN-2002
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E2 protein (
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Q9Z068;
Q1-MAY-1999
Q1-MAY-1999
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NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98411405; PubMed=9738045; Mizuno M., Higuchi T., Kanmatsuse K., Esumi M.; "Genetic and serological evidence for multiple unrecognized transmission of hepatitis C virus units.";
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-CT-2002 (TrEMBLrel. 22, Last sequence update)
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E2 region (Genome polyprotein) (Fragment).
Hepatitis C virus.
Viruses, ssRNA positive-strand viruses, no DNA st
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STRAIN=R4C10;
Gaudy C., Moreau A.,
 Hepatitis
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NCBI_TaxID=11103;
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InterPro; IPR002531; HCV_NS1.
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Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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"Pretreatment analysis of HCV-1b HVR1 amino acid sequences to
differentiate strains resistant and sensitive to antiviral therapy."
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF473772; AALB6842.1; -.
InterPro; IPR002531; HCV NS1.
Pfam; PF01560; HCV NS1; I.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmebrane.
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NON_TER 27 27
SBQUENCE 27 AA; 2702 MW; A7F6C7F44073C4D5 CRC64;
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Q9J5Y5;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2002 (TrEMBLrel. 22,
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NCBI_TaxID=11103;
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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NON TER
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SEQUENCE 27 AA; 2852 MW; 0
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J. Virol. 74.4327-4334(2000).
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MEDLINE=20219428; PubMed=10756048;
MADZIN A., Solforosi L., Debiaggi M.,
Zanetti A.R., Clementi M.;
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STRAIN=R4C8;
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100.0%; Pred. No. 3.2e+02;
ative 0; Mismatches 0;
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6FCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/backfīles1.pep:*
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US-08-667-073-898-67

US-09-073-898-67

US-09-339-511-1

US-09-339-511-3

US-09-339-511-4

US-09-339-511-4

US-09-339-511-3

US-08-861-476C-3

US-08-861-476C-3

US-08-466-552A-10

US-08-466-552A-10

US-08-468-552A-10

US-09-201-945-201

US-09-201-945-201

US-08-156-252A-19

US-09-201-945-153

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US-09-201-945-153

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US-09-141-992-56

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34.252 Million cell updates/sec
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APPLICANT: Mayville, Patricia
APPLICANT: No. 6337385ick, Richard P.
ITILE OF INVENTION: NOVEL: STAPHYLOCOCCUS PEI
TILLE OF INVENTION: NOVER: US/09/339,511
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEG ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEG ID NO 8
LENGTH: 5
                                                                                                                 US-08-960-780-67

; Sequence 67, Application US/08960780

; Patent No. 6204455
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                 Sequence 67, Application of the control of the cont
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US-09-339-511-8
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Matches 4
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Conservative
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US-08-818-253-48
US-09-094-359-16
US-09-172-063-36
US-09-172-063-36
US-09-18-252-48
US-09-49-95-14
US-09-316-919-21
US-08-789-335F-24
US-09-169-015-34-23
US-09-169-015-72-5
US-08-787-738B-24
US-09-18-77-748-26
US-09-18-77-748-26
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US-09-18-77-748-27
US-09-18-77-75-75-75
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                                                                                                                                                                                                                                                                                           Patent No.
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide TITLE OF INVENTION: Sequences Which Encode These Toxins NUMBER OF SEQUENCES: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 1:
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FILING DATE: 30-OC
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.30
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                                                               INVENTION:
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                             Morrill, George
Finstad-Lee, Stacey
Finstad-Lee, Stacey
VENTION: No. 6242669el Pesticidal Toxins and Nucleotide
VENTION: Sequences Which Encode These Toxins
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Dullum, Charles Joseph
Muller-Cohn, Judy
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Schmeits, James
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Saliwanchik, Lloyd & Saliwanchik
21 N.W. 41st Street, Suite A-1
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Best Local Similarity
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; MOLECULE TYPE:
US-09-073-898-67
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Patent No. 6337385
GENERAL INFORMATION:
                                                                                                                                                   SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                     CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
                                                                                                                                                                                                                                       FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: No. 6337385ick, Richard
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                                                                                                                                                                                      NUMBER OF SEQ ID NOS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 60/
FILING DATE: 30-OCT-1996
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 30-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                 OTHER INFORMATION:
OTHER INFORMATION:
                                                                                   FEATURE:
                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                       PPLICANT: Ji, Guangyong
ITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
ITLE OF INVENTION: INTERFERENCE
                                                                                                                                     ENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                  AME/KEY: VARIANT
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STATE: FL
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REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA
REFERENCE/DOCKET NUMBER: MA
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INFORMATION: Xaa represents any amino acid
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30-OCT-1997
                                               Description peptide
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                                                                 Artificial Sequence:
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; CIHER INFORMATION: Xaa represents any amino acid at this position US-09-339-511-2
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SOFTWARE:
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SEQ ID NO 2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/339,511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
                                                                               CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRGANISM: Artificial Sequence
                                                                                                                          PPLICANT: Ji, GLANGYONG
TILS OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
ITLE OF INVENTION: INTERFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LICANT: Ji Guangyong
LE OF INVENTION: NOVEL STAPHYI
LE OF INVENTION: INTERFERENCE
E REFERENCE: 600-1-231N
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5337385
                   PatentIn
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Mayville, Patricia
No. 6337385ick, Richard
                                                                                                                                                                                                                                                                  Application US/09339511
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No. 6337385ick, Richard P.
Beavis, Ronald
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Conservative
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SEQ ID NO 4
LENGTH: 9
TYPE: PRT
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Best Local Similarity
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Best Local
SEQ ID NO
                          GENERAL INFORMATION:

APPLICANT: New York University Medical Center

TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS

FILE REFERENCE: 63753/7

CURRENT APPLICATION NUMBER: US/08/861,476C

CURRENT FILING DATE: 1997-05-22

NUMBER OF SEQ ID NOS: 8
                                                                                                                                                 Sequence 3, Application US/08861476C Patent No. 6447786
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Patent No. 6337385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/339,511
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHY
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                SOFTWARE:
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LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
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Best Local S
Matches 4
                                             Sequence 43, Application Patent No. 5817748
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Best Local Similarity
                                                                         08-406-330-43
                                                                                                                                                                                                                                                                                                                     TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 02-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 15-NOV-19
                                                                                                                                                                                                                                                                                                                                                           NAME: LOGAN, APTIL C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: SC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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APPLICANT: Curnutte, John
TITLE OF INVENTION: REGULA
TITLE OF INVENTION: LMWG-I
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STREET: La Jo.
CA
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CORRESPONDENCE ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION:
CANT: Miller, Jonathan L.
CANT: Lyle, Vicki A.
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10666 No. 5726155th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                       12 amino acids
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100.0%; Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 201, Application US/08637759B Patent No. 5876931
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                                                                                                                                                                                                                                                                                                                                                                                                      atent No. 5876931
GENERAL INFORMATION:
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                                                                                                                                               COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: FROM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,330
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: David W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                    CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rochester
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSLF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                    Georgia
                                                                                                                                                                                                                                                                                     2800 One Atlantic Center
1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Nixon, Hargrave, Devans & Doyle Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 amino acids
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100.0%; F1
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                                                                                                                                                                                                                                                                                                                                                                      Identification of Genes
                                                                                                                                                                                                                                                                                                                                                         501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20884/100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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ATTORNEY/AGENT INFORMATION:

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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-556-597-43:
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; HYPOTHETICAL:
US-08-637-759B-201
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 201:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                              TELEPHONE: (716) 263-1636
TELEPAX: (716) 263-1600
[INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                NAME: Tinian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPPLICANT: Miller, Jonathan L.
NPPLICANT: LYle, Vicki A.
NITLE OF INVENTION: MIMOTODES AND ANTI-MIMOTODES OF
NITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
                                                                                                STRANDEDNESS:
                                                                                                                LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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 94.7%;
100.0%;
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quare, P.O. Box 1051
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100.0%; Pred. No. 66;
tive 0; Mismatches
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   Score 18;
Pred. No.
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   DB 2;
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                Length 12;
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US-09-035-249A-10
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                                                                                                                                                                                                                                                                                                                                                                     US-08-871-355A-201
                                                                                                                       Sequence 10, Application US/09035249A Patent No. 6184203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 201, Application US/08871355A
Patent No. 6015669
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (404) 873-879
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/871,355A
                          APPLICANT: Bokoch, Gary M
APPLICANT: Curnute, John T
TITLE OF INVENTION: REGULATION OF OXIDATIVE BURST USING
TITLE OF INVENTION: LAMG-DERIVED PEPTIDES AND ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                      No.
                                                                                                                                                                                                                                                              2 SSLF 5
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: Georgia
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                                                                                                                                                                                                                                                                                              4; Conservative
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/ENTION: Identification of Genes
                                                                                                                                                                                                                                                                                                                                                                               , protein
NO
                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                 94.7%; Score 18;
100.0%; Pred. No.
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RESULT 15
US-09-201-945-201
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Best Local Similarity 100.
"---hes 4; Conservative
                                                                                                                                                                                         DAVIG WILLIAM Holden

LILE OF INVENTION: Identification c
NUMBER OF SEQUENCES: 501

CORRESPONDENCE ADDRESS:
ADDRESSEE: Patreat. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
COUNTRY: USA
ZIP: 30309-217
VPUTFF 30309-217
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 201, Application US/09201945
Patent No. 6342215
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,552
FILING DATE: 15-NOV-1993
APPLICATION NUMBER: US 08/102,944
FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: LOGAN, ADXILC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 619-554-2937
TELEPAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: LOGAN, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 100.
                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/035,249A FILING DATE: CLASSIFICATION:
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10666 No. 6184203th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                            David William Holden
VENTION: Identification of Genes
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Pred. No.
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                            Query Match
Best Local Similarity lvv.
Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: PABST, PATTER I.
REGISTRATION UNMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1873-8794
                                                                                                                                                                                   TELEFAX: (404) 873-879.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                          ELEPHONE: (404) 873-8795
PELEFAX: (404) 873-8795
PELEFAX: 750 TD NO: 201:
                                                                                                                                                : YEOLOGY:
                                                                                                                                                                     ENGTH: 12 amino acids
                                                                                                                                                        RANDEDNESS:
                   2 SSLF 5
SSLF 11
                                                                                                                                         uss: single
linear
                                                                                                                  .: protein
                                            94.7%; oc.
100.0%; Pr
                                                              Score 18; DB 4; Length 12; Pred. No. 66;
                                                 Mismatches
                                                 0; Indels
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Gaps

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Search completed: January 29, 2004, 15:03:23 Job time : 7.17647 secs

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Result
No.
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using
                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                           Score
       Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
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Match Length
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Copyright (c) 1993 - 2004 Compugen Ltd
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US-10-032-950-1

US-10-032-950-2

US-10-032-950-3

US-10-032-950-4

US-10-201-444-3

US-10-201-444-3

US-10-293-086-12

US-10-293-086-12

US-10-097-175-86

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US-10-300-6941-5

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US-10-174-613-31
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US-10-022-066-231
US-09-850-351A-67
US-10-022-066-266
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               Sequence 8, Appli
Sequence 231, App
Sequence 67, App
Sequence 266, App
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 470, App
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 15, Appli
Sequence 16, Appli
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4.5	44	43	42	41	40	39	8	37	36	(J.)	34	33	32	L)	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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-09-999-745-21	S-10-029-386-32	S-09-882-171-36	S-09-809-391-36	-09-833-245-37	-10-023-282-10	-10-253-471-60	-09-962-756-60	-09-933-767-10	0-253-471-7	-10-253-471-74	-10-253-471-74	0-253-471-74	S-09-962-756-74	9-962-756-74	S-09-962-756-7 4	S-09-962-756-74	S-09-820-649-33	S-10-160-162-33	S-09-776-724A-22	4-761-41	-09-864-761-3725	S-09-866-066-2	-09-864-761-4086	-10-225-567A-1	S-10-062-831-8	S-10-062-599-8	-09-759-01	-10-158-847-5	S-10-158-825-
quenc	equenc	equence	equence 3	equence 3	equence 1	equence 6	equence 6	equence 10	equence 74	equence 74	equence 74	equence 74	equence 74	equence 7	equence 74	equence 74	equence 33	equence 33	equence 22	nce 41	equence 372	ce 28	quence 40	ence 16	equence 88	equence 8	. Sequence 10,	equence 5	quence

ALIGNMENTS

RESULT 1 US-10-032-950-8

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Publication No. US20020077453A1
GENERAL INFORMATION:
APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: Mo. US20020077453A1ick, Richard
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
                                                                                                                                                                                                                                                                                                                                                                                                            US-10-032-950-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ji, Guangyong
TITLE OF INVENTION: INVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 5
                                                                                                                                                                                                 Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (1)
OTHER INFORMATION: Xaa represents any amino acid at this position of the control of the cont
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SSLF 5
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100.0%; Pred. No. 6.9
tive 0; Mismatches
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; Sequence 67, Applicati
; Patent No. US200201000
; GENERAL INFORMATION:
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US-10-022-066-231
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/022,066
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/256,410
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/256,409
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HILDEBRAND, WILLIAM H.
APPLICANT: PRILLIMAN, KILEY RAE
TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 6680.034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/974,366
PRIOR FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/465,321 PRIOR FILING DATE: 1999-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO 231
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                               NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                  MOTTILI, George
TITLE OF INVENTION: No. U820020100080A1el Pesticidal Toxins and Nucleotide
Sequences Which Encode These Toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 SSLF
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4; Conservative
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                                                                                                                                             COUNTRY: US
                                                                                                                        ZIP: 32606-6669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09850351A
                                                                                                                                                                                                                                                                                                                                          Loewer, David
Dullum, Charles Joseph
Muller-Cohn, Judy
Stamp, Lisa
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Stockhoff, Brian A.
Schmeits, James
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Pred. No.
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                     Version #1.30
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CURRENT APPLICATION NUMBER: US/10/022,066
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/256,410
PRIOR FILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/256,409
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/465,321
PRIOR APPLICATION NUMBER: 09/465,321
PRIOR FILING DATE: 1999-12-17
PRIOR APPLICATION UMBER: 09/974,366
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE DESCRIPTION: SEQ ID NO: 67: US-09-850-351A-67
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                                                                                                                                              US-10-022-066-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: HILDEBRAND, WILLIAM H.
APPLICANT: PRILLIMAN, KILEY RAE
                                                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 266, A
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Best Local Similarity 100.0%; Pred. No. Matches 4; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PRILLIMAN, KILEY RAE
TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 6680.034
                                                                                                                                                              FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION
                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/073,898
FILING DATE: 06-MAY-1998
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-CCT-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-CCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708CD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MATION FOR SEQ ID NO: 67: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
2 SSLF 5
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/850,351A FILING DATE: 07-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sanders, Jay M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELEFAX: 352-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/10022066
                                                           94.7%; Score 18; DB ilarity 100.0%; Pred. No. 6.: Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US20030166057A1
                                                                                                                                                              Description of Artificial Sequence: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                               DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
. 6.9e+05;
                                                                                                  Length 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
1, DO 2
1, DO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Beavis, Ronald
APPLICANT: J1, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-211N
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/032,950 CURRENT FILING DATE: 2001-12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
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APPLICANT: No. US20020077453A11ck, Richard
                                                                                                                                                                                                                                                                                                                                                                      PPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERPERENCE
TILE REFERENCE: 600-1-231N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             equence 2, Application US/10032950 iblication No. US20020077453A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OFTWARE: PatentIn Ver. 2.0
OTHER INFORMATION: Xaa represents any amino acid at this position
                     OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: peptide
NAME/KEY: VARIANT
LOCATION: (5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                       ORGANISM: Artificial Sequence
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4; Conservative 0;
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No. US20020077453Alick, Richard P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beavis, Ronald
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100.0%; Pred. No.
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APPLICANT: No. US20020077453Alick, Richard
APPLICANT: No. US20020077453Alick, Richard
APPLICANT: No. US20020077453Alick, Richard
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEP
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
COMMENCE: Details 1998-06-24
                                                                SEQ ID NO 4
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
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                                                                                   CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                       APPLICANT: Muir Tom
APPLICANT: Muyville, Patricia
APPLICANT: Mo. US20020077453A1ick, Richard P.
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
                                                                                                                                                                                                                         APPLICANT: J1, Guangyong
TITLE OF INVENTION: NOTEL STAPHYLOCOCCUS PEPTIDES
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position.
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
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100.0%; Pred. No.
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US-09-572-270A-470
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                                                                                                                                  ) ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in Unknown at 10-19 and may interact with
US-09-572-270A-470
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Best Local S
Matches 4
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Best Local S
Matches 4
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CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 1144
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 470
                                                                                                                                                                                                                                                                                                               Publication No. US20030148368A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Inter- complementary peptide listing
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                                                                   Matches
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Best Local Similarity
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CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US/08/861,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: New York University Medical Center TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS FILE REFERENCE: 63753/7
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NUMBER OF SEQ ID NOS: 8
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OTHER INFORMATION:
OTHER INFORMATION:
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100.0%;
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; Pred. No. 1.8e+02;
                                                                   Mismatches
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; OTHER INFORMATION: Androgen Receptor Binding Polypeptides
US-10-097-175-86
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Best Local S
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APPLICANT: JOYAL, J
APPLICANT: MUBLLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12 LENGTH: 11
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SEQ ID NO 86
LENGTH: 11
                                                           Query Match
Best Local Similarity
Matches 4; Conserv
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TITLE OF INVENTION: Cellular Kinase Targets and Inhibitors,

TITLE OF INVENTION: and Methods For Their Use

FILE REFERENCE: 50036/048002

CURRENT APPLICATION NUMBER: US/10/293,086

CURRENT FILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: US 60/337,990

PRIOR FILING DATE: 2001-11-13

NUMBER OF SEQ ID NOS: 144
                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/352,399
PRIOR FILING DATE: 2002-01-28
NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: PPI-110
CURRENT APPLICATION NUMBER: US/10/097,175
CURRENT FILING DATE: 2002-03-12
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/275,240 PRIOR FILING DATE: 2001-03-12 PRIOR ADDITORMON
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APPLICANT: FINDEIS, MARK A.
TITLE OF INVENTION: PEPTIDIC MODULATORS OF
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                   TYPE: PRT
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No. US20030134310A1
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Pred. No.
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Pred. No.
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2e+02;
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RESULT 13 US-10-435-666-1

; Sequence 1,
; Publication

Application US/10435666 No. US20040006001A1

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CURRENT APPLICATION NUMBER: US/10/435,666
CURRENT FILING DATE: 2003-05-12
PRICK APPLICATION NUMBER: 60/379,145
PRIOR FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1
LENGTH: 12
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Middleton, Crystan
TITLE OF INVENTION: INVERFACIAL BIOMATERIALS
FILE REFERENCE: 180/143/2
CURRENT APPLICATION NUMBER: US/10/300,694A
CURRENT FILING DATE: 2003-05-07
PRIOR APPLICATION NUMBER: US 60/331,843
PRIOR FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 117
SOFTWARE: Patentin version 3.2
SEQ ID NO 5
SEG ID NO 5
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US-10-435-666-1
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US-10-174-613-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Polystyrene-binding peptide 5 US-10-300-694A-5
Sequence 31, Application US/10174613
Sequence 31, Application US/10174613
Publication No. US20030114354A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL POTASSIUM CHANNEL WITH HOMOLOGY
TITLE OF INVENTION: Ether-a-go-go FAMILY, HEAG2
FILE REFERENCE: D0123 NP
CURRENT APPLICATION NUMBER: US/10/174,613
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US 60/299,378
PRIOR APPLICATION NUMBER: US 60/299,378
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APPLICANT: CARTER, Daniel C.
TITLE OF INVENTION: FERRITIN FUSION PROTEINS FOR USE IN VACCINES AND OTHER APPLICATIC
FILE REFERENCE: P07624W000/BAS
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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APPLICANT: Duke University
APPLICANT: Grinstaff, Mark W.
APPLICANT: Kenan, Daniel J.
APPLICANT: Walsh, Elisabeth B.
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ORGANISM: Artificial
FEATURE:
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100.0%; Pred. No. 2.4e+02;
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                                                                                                ; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-613-31
                                                Matches
                                                                                                                                                SOFTWARE: P
                                                            Query Match
Best Local Similarity
                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/300,614
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 93
 1 SSLF 4
                         2 SSLF 5

    Conservative

                                                                                                                                                               PatentIn version 3.0
                                                            94.7%;
100.0%;
                                                            Score 18; DB 15;
Pred. No. 2.4e+02;
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Search completed: January 29, 2004, 15:01:47 Job time : 15.1912 secs